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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916 C;Comment: This protein may be involved in the oncogenic potential of this virus. C;Superfamily: papillomavirus E6 protein C;Kuperfamily: papillomavirus E6 protein C;Kupwords: DNA binding; early protein; zinc finger F;30-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translation n
A;Molecule type: DNA
A;Residues: 1-149 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A32444
R; Goldsborough, M.D
Virology 171, 306-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: host domo sapiens (man) C;Date: 31-Mar-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E6 protein - human papillomavirus type 31 C;Species: human papillomavirus type 31 A;Note: host .omo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc
A;Reference number: A94398; MULD:89299478; PMLD:2545036
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005172; NID:g5103820; PIDN:AAD39650.1; GSPUB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-1451 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                           15 LSSALEIPYDE 25
                                                                                                                       1 LSXELXIPYEE 11
                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T. 171, 306-311, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation not shown
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                                                                                                                                                                                      Conservative
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    Mismatches

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                                                                                                                                                                                                                 Score 35; DB 1; Length 149; Pred. No. 5.1;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosci. Biotechnol. Biochem. 64, 1416-1421, 2000
A;Title: Pyrithiamin resistance gene (ptrA) of Aspergillus oryzae: Cloning, characte.
A;Reference number: JC7337; MUID:20399355; PMID:10945258
                                                                                                                                                                                                                                        hypothetical protein ORF102 - Lymantria dispar nuclear polyhedrosis virus C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMMPV C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C;Accession: T30452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein BB0267 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #scquence_revision 13-Feb-1998 #text_change 08-Oct-1999
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A; Residues: 1-327 < KUB>
A; Molecule type: DNA
A; Residues: 1-381 < KUZ>
                                                                                   A; Reference number: 220836; MUID:99124785; PMID:9887315
A; Accession: T30452
                                                                                                                                                                            R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; + Virology 253, 17-34, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-634 <KLE>
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A; Accession: C70133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme discase spirochaete, Borrelia burgdorferi
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                                                                                                                                           A; Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri
                                                                                                                                                                                                                                                                                                                                                                             T30452
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                                 preliminary; translated from GB/EMBL/DDBJ
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6; Conserv
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G.; Clayton, R.; Lathigra, R.; WI
J.; Salzberg, S.; Hanson, M.; Yo
Horst, K.; Roberts, K.; Hatch, B

Score 35;

DB 2; Length 327;

Pred.

Mismatches NO.

0;

0

Score 35; DB 2;

Length 634;

Pred. No. 26;

Mismatches

0;

Gaps

0;

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RESULT 10

A;Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70288.1; PID:g3822337

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A;Map position: 1
C;Superfamily: DNA-directed DNA polymerase I
C;Keywords: nucleotidyltransferase
                                                                                                                                     A;Residues: 'MVFCCDGGLSCESIDFALCCLRGRSGNYVQSRILP',1-12,'T',14-41,'H',43-72,'F',74-92,'P'A;Cross-references: GB:AE002012; GB:AE000513; NID:g6459473; PIDN:AAF11264.1; PID:g645947A; PID:g6459473; PIDN:AAF11264.1; PID:g645947
                                                                                                                                                                                                                                                                                                                                            R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mass.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A40597; MUID:93273728; PMID:8501062
A;Accession: A40597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed DNA polymerase (EC 2.7.7.7) I - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans C;Dete: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-2000 C;Accession: A40597; F75363; S42112; S42235
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A; Introns: 201/3; 221/3; 287/1; 410/3; 551/1; 672/3; 723/3
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A;Molecule type: DNA
A;Residues: 1-738 <WIL>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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                                                                                         A; Gene: DR1707
                                                                                                                   C; Genetics
                                                                                                                                                                                                                                                            A; Accession: E75363
                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L14581; NID:g290067; PIDN:AAC36974.1; PID:g290068
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Gutman, P.D.; Fuchs, P.; Ouyang, L.; Minton, K.W. J. Bacteriol. 175, 3581-3590, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Caenorhabditis elegans hypothetical protein Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T27289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Matthews,
                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-921 <GUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL032622; PIDN:CAA21499.1; GSPDB:GN00021; CESP:Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z20338
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75.0%;
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    Mismatches

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Pred. No. 50;
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Search completed: January 15, 2003, 12:37:13
Job time : 19.1429 secs
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AB1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein lin0057 [imported] - Listeria innocua (strain Clip11262) C; Species: Listeria innocua
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                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL592022; PIDN:CAC95290.1; PID:g16412478; GSPDB:CN00178
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294, 849-852,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Jones,
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                                                                                                                                                                                         Matches
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Matches 7; Conservative
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Pred. No. 65;
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Copyright (c) 1993 - 2003 Compugen Ltd
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CG18_YEAST
VE6_HPV31
THI4_ASPOR
DPO1_DEIRA
        ACKA_HELPJ
NEC1_RAT
NEC1_HUAN
DP01_THEF1
CLAA_BACTU
AROE_HELPJ
TH14_AERPE
MTAP_CAEELL
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IDI1_HUMAN
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                         0 rattus norv
10 homo sapien
15 thermus fil
16 bacillus th
18 helicobacte
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 HSSP; P19821; 1:ray,
InterPro; IPR002441; 5_3_exonuclease.
InterPro; IPR00198; DNA_pol.
InterPro; IPR00198; DNA_pol.
InterPro; IPR002298; DNA_pol.
InterPro; IPR003513; Exo_N_I.
InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
InterPro; IPR003584; HHH_2.
InterPro; IPR003584; HHH_2.
InterPro; IPR001532; XPGC_Rad.
InterPro; IPR001532; XPGC_Rad.
IPGam; PF00476; DNA_pol_A; 1.
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF01367; 5_3_exonuc_N; 1.
R PRINTS; PR00868; DNAPOLI.
R PRINTS; SM00475; 53EXOC; 1.
R SMART; SM00475; 53EXOC; 1.
SMART; SM00475; 53EXOC; 1
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
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29muv5	P13026	094751	Q58446	Q9ntn9	052720	084309	Q9z992	Q9pk86	Q57484	P52924	P40998
mesostigma	hungarian g	schizosacch	methanococc	homo sapien	klebsiella	chlamydia t	chlamydia p	chlamydia m	haemophilus	saccharomyc	schizosacch

## ALIGNMENTS

USE	ESULT 1
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Ο	Thermus thermophilus.
( )	Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
( )	
×	NCBI_TaxID=274;
2	[1]
70	SEQUENCE FROM N.A.
( )	STRAIN=ACM B-1257;
×	MEDLINE=93087201; PubMed=1454544;
1 12	
	moternate trouting and nationated sequence of the big portinetes gene from Theorems 1.
ς,	Nucleic Acids Res. 20:5839-5839(1992).
( )	-1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
( )	1
( )	-!- BIOTECHNOLOGY: Used in the PCR method because of its high
( )	
()	-!- MISCELLANFOUS: Has an optimal temperature above 70 degrees
( )	Celsius; can be used at temperatures up to 95 degree Celsius.
. ()	-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
1 (1	
2 (2	This SWISS-PROT entry is copyright. It is produced through a collaboration
) (	ween the Swiss institute of Bioliformatics and the EMBL Outstatio
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P19821;
                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832.
MEDLINE-96016150; PubMed-7568114;
MODOLEV S., Nayal M., Barnes W.M., di Cera E., Waksm "Crystal structure of the large fragment of Thermus polymerase I at 2.5-A resolution: structural basis thermostability.";
                                                                                                                                                                                                                                    MEDLINE=95364959; PubMed=7637814;
Kim Y., Eom S.H., Wang J., Lee D.-S., Suh S.W., Steitz T.A.;
"Crystal structure of Thermus aquaticus DNA polymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991
01-FEB-1991
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                                                                Eom S.H., Wang J., Steitz T.A.; "Structure of Tag polymerase with DNA Nature 382:278-281(1996).
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MEDLINE-89197950; PubMed-2649500;
Stoffel S., Saiki R.K., Myambo K.,
 complexes
                                X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
MEDLINE-99077817; PubMed-9857206;
                                                                                                                             [5] Natl.
                                                                                                                                                                                                                                                                                                                                          MEDLINE=95204371; PubMed=7896728; Ishino Y., Ueno T., Miyagi M., Ue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus aquaticus
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"Crystal structures of open and closed forms of binary and ternary complexes of the large fragment of Thermus aquaticus DNA polymerase
                                                                                                    MEDLINE=96353982; PubMed=8717047;
                                                                                                                X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                              Nature 376:612-616(1995).
                                                                                                                                                                                                                                                                                                                                   Kato I.;
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-YT
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation, characterization, and expression in Escherichia coli the DNA polymerase gene from Thermus aquaticus.";
J. Biol. Chem. 254:6427-6437(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase I,
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01-FEB-1991 (Rel.
15-JUN-2002 (Rel.
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TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                    "Overproduction of Thermus aquaticus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                         -RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                       Y., Korolev S., Waksman G.;
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                                                                                                                                                                                                                                                                                               analysis by ion-spray . 116:1019-1024(1994).
                                                                                                                                     Acad. Sci. U.S.A. 92:9264-9268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus.
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17, Last sequence update)
41, Last annotation update)
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93783 MW;
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Pred. No. 0.19;
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between
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ALD DARWER RESERVED TO THE RES

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SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1
                                                                                                                                                                                                                                                                                                        Pfam; PF00476; DNA_pol_A; 1.epfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.eprints; PR00868; DNAPOLI.smart; SMO0475; 53EXOC; 1.exonuc_N; 1.exonuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
        PROSITE: PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; 3D-structure.
DNA-binding; 3D-structure.
DNA-IN 410 832 POLYMERASE (BY SIMILARITY).
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Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99380545; PubMed=10449720; Li Y., Mitaxov V., Waksman G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) MEDLINE-98266352; PubMed-9605316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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80 J. 17:7514-7525(1998).
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SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
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D32013;
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22-DEC 99.
22-DEC 99.
22-DEC 99.
30-SEP 98.
14-OCT 98.
12-MAR-97.
16-AUG-99.
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16-AUG-99.
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11-APR-97.
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BAA06775.1;
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POLYMERASE (BY SIMILARITY)
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PROPERTY OF STANDARD 
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Best Local
                                                                                                                                       Pfam; PF00476; DNA_pol_A; 1.
Pfam; PF01367; 5.3_exonuclease; 1
Pfam; PF02739; 5.3_exonuclease; 1
Pfam; PF02739; 5.3_exonuclease; 1.
PRINTS; PR00868; DNAPOLI.
SNART; SM00475; 53EXOc; 1.
SNART; SM00278; HhH1; 1.
SNART; SM00279; HhH2; 1.
SNART; SM00279; POLAC; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_polI.
InterPro; IPR000513; Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Submitted (AUG-1996)
                                                                                                                   TIGRFAMS; TIGR00593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U62584; AAB81398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Bic., em., 214:135-140(1993).
-- FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE
--- ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY.
--- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate -- N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93285135; PubMed=8508785; Park J.H., Kim J.S., Kwon S.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus caldophilus.
Bacteria; Thermus/Deinococcus
                                           Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                   PROSITE; PS00447; DNA_POLYMERASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003583; HHH_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P19821; 1TAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and characterization of Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GK24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=272;
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93909 MW;
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.19;
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F1731055B5246F03 CRC64;
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Best Local s
Matches
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                                                                                                                    PRINTS; PRO0868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                             Pfam; PF00476; DNA_pol_A; 1. Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
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SEQUENCE
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01-OCT-1996 (Rel.
15-JUN-2002 (Rel.
                                                                       DNA-binding.
                                                                                                           TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, nucleotide sequence, and expression in Escherichia coli of DNA polymerase gene (polA) from Therms thermophilus HBB.";

J. Ferment. Biceeq. 76:265-269(1993)

-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate — N diphosphate
                                                 SEQUENCE
                                                            DOMAIN
                                                                                 Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                               TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                     InterPro; IPR003584; HHH_2
                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
use by non-profit institutions as 1
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urabe I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asakura K., Komatsubara H., Soga S., Yomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPOT_THETH
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  Similarity
9; Conser
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IPR000513;
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                                                                                                                                                                                                                                                                 1PR001098; DNA_FOI
                                                                                                                                                                                                                                                                              IPRO02421; 5_3_exonuclease.
                                                834 AA;
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  Conservative
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93798 MW;
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            93.6%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                               institutions as long as its content
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                     Score 44; DB 1;
                                                          POLYMERASE (BY SIMILARITY)
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Pred. No. 0.19;
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                                              1A98145DC11A54A9
Mismatches
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1 LSXELXIPYEE 11

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RESULT 6

VE6_HPV31

ID VE6_J
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AC P1731

AC P1731

DT 01-AL
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DE E6 E1
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OS HUMBAL
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CG18_YEAST
P38794;
                                                                      VE6_HPV31
P17386;
O1-AUG-1990
O1-AUG-1990
15-JUN-2002
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01-FEB-1395 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
G1/S-specific cyclin PCL5.
PCL5 OR YHE 71W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
Papillomavirus
           Viruses; dsDNA viruses,
                        Human papillomavirus
                                                                                                                                                                                                                                                                                                                                           Cyclin; Cell cycle; Cell division. SEQUENCE 229 AA; 26467 MW; B68
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geiseel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S46696; S46696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-SPECIFIC CYCLINS. PCE1 AND PCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                 174 LNYELAIPYDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0001113; PCL5.
InterPro; IPR004366; Cyclin.
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7; Conserve
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(Rel. 41, Last ann
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                        type
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         pe 31.
no RNA stage; Papillomaviridae;
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ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                     Biosci. Biotechnol. Biochem. 64:1416-1421(2000).

1. FUNCTION: INVOLVED IN BIOSYNTHESIS OF WHE THIAMI
THIAKOLE (BY SIMILARTY).

1. SUBCELLULAR LOCATION: Mitochondrial (Potential).

1. SIMILARTY: BELONGS TO THE THI4 FAMILY.
This SW155 :.... The between the Swiss Institute or the European Bioinformatics Institute. The European Bioinformatic Institutions as long the monte of the swiss and the swiss are the 
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rubodera T., Yamashita N., Nishimura A.;
"Pyrithiamine resistance gene (ptrA) of Aspergillus oryzae: cloning,
characterization and application as a dominant selectable marker for
transformation.";
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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bloinformatics and the EMHL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus."; Virology 17:1306-31(1989).
-I- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
-I- FUNCTION: EXHABIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMEL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiazole biosynthetic enzyme, mitochondrial precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HL1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5062;
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149 AA;
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OSYNTHESIS OF WHE THIAMINE PRECURSOR
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l; Mismatches
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DPO1_DEIRA
P52027;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
-i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE ACTIVITY (HY EXHIBITS 3, TO 5, AND 5, TO 3, EXONUCLEASE ACTIVITY (HY
                                                                                                                                                                                                                                                                                                                                                MEDLINE-20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Feterson J.D., White O., Elsen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L., Dodson R.J., Haff D.H., Gwinn M.L., Nelson W.C., Shen M., Shen M., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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SEQUENCE
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01946; Thi4; 1.
TIGRFAMS; TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification, sequencing, and targeted mutagenesis of polymerase gene required for the extreme radioresistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    Fraser C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gutman P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE * 93273728; PubMed = 8501062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Thermus/Deimococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLA OR DR1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF217503; AAF25444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ELGVPYEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 175:3581-3590(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ELXIPYEE 11
                                                                                                                                              SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                              SIMILARITY).
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                  [DNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis; Mitochondrion; Transit peptide; FAI

MITOCHONDRION (POTENVIAL).

P 327

THIAZOLE BIOSYNTHETIC ENZYME.

P 107

FAD OR NAD (POTENVIAL).

327 AA; 35099 MW; 7C561EE06742B2AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36-956 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuchs P., Ouyang L., Minton K.W.;
                                                                                                                                                                   SINGLE-CHAIN MONOMER WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.4
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          956
                                                 There are no restrictions ong as its content is in
                                                                                                                                                                   MULTIPLE FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 327
                                                                                                                                                                                                                                                             THIS DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD.
                                                                                                                                                                                                                                                                                                                                                                       R.D.
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RESULT 9
THI4_YEAST
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00476; DNA_Pol_A; 1.
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonucle,; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM0028; POLAC; 1.
                                                                                                                                                                                                                                                                                                         P32318;
01-0CT-1993 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
CONFLICT
The sequence of a 27 kb segment on the right arm of chromosome from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, PEM1/CHO2, NSR1 genes and ten new open resistance.
                                                                                                                                                                                                                                                               01-007-1993 (Rel. 27, Created)
01-007-1993 (Rel. 27, Last sequence update)
16-007-2091 (Rel. 40, Last annotation update)
Thiazole biosynthetic enzyme, mitorhondrial precursor.
"H14 OR MOLI OK ESP35 OR YUK144W OR G6620.
                                    MEDLINE~96158062; PubMed~8585325; Skala J., Nawrocki A., Goffeau A.
                                                                                                                                                                    Praekelt U.M., Meacock
"MOL1, a Saccharomyces
                                                                                                                                                                                                                        Saccharomycetales; NCBI_TaxID-4932;
                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Haker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                            STRAIN-S288c
                                                                                       Nawrocki A., del Bino S., Goffeau A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                          early
                                                                                                                                                                             MEDLINE=93070608; PubMed=1441749;
Praekelt U.M., Meacock P.A.;
                                                                   SEQUENCE OF 205-326
                                                                                                               van Dyck
                                                                                                                                              Yeast
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  THI4_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000513; Exo_N
InterPro; IPR003583; HHH_1
InterPro; IPR003584; HHH_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                      803 LSNDLGIPYAE
                                                                                                                                                                                                                                                                                                                                                                                                            1 LSXELXIPYEE 11
                                                                                                                                       stationary phase during growth on molasses."; 8:699-710(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P19821; 2KTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE002012; AAF11264.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L14581; AAC36974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
7; Conserv
                                                                                                   A L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR00593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1PR001098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPK002421;
                                                                                                 Skala J.,
del Bino
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                      813
                                                                                                             ٦.,
                                                                   FROM
                                                                                                                                                                                                                                 Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXO_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                           72.3%;
63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pola;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5_3_exonuclease.
                                                                                                 de Wergifosse
S., Goffeau A.;
                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -binding: Complete p
T -> A (IN KEF: 1)
H -> D (IN KEF: 1)
F -> L (IN REF: 1)
P -> R (IN REF: 1)
P -> R (IN REF: 1)
P -> R (IN REF: 1)
C -> V (IN REF: 1)
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 26;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6ABBF117D75AB84A
                                                                                                           ₽.,
                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                            Purnelle B., Talla
                                                                                                                                                                                                                                                                                                                                ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair;
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[F]
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                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MCEA_SYNY3

ID MOEA_SYNY3

ID MOEA_SYNY3

AC Q55368

AC Q55368

OT 01-NOV
DT 01-NOV
DT 16-OCT
DE MO1ybd
GN MOEA O
OS Synech
OC Bacter
OC MCBL_T
RN [1]

RP SEQUEN
RX MEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                       01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                           Synechocystis sp. (strain Bacteria; Cyanobacteria; C
                                                                                                                                            Molybdopterin biosynthesis protein moeA. MOEA or SIR0900.
                      SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=1148;
                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                                                                                                                                                                 Q55368;
                                                                                                                                                                                                                                                                                             MOEA_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: EXPRESSED AT HIGH LEVELS IN THE PHASE OF BATCH CULTURES GROWING ON MOLASSES, AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    damage tolerance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Machado C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98035046; PubMed=9367751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Praekelt U.M., Byrne K.L., Meacock P.A.;
"Regulation of THI4 (MOL1), a thiamine-biosynthetic gene
Saccharomyces cerevisiae.";
  MEDLINE~96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION IN DNA DAMAGE TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Dual role for the yeast THI4 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast 10:481-490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95028146; PubMed=7941734;
                                                                                                                                                                                                                                                                                                                                                                                                                   128 ELEIPYED 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THIAMINE REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 11:1421-1427(1995)
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3L; X51669; CAAA3843.1; -.

11; X5807; CAA59802.1; -.

12; Z72929; CAA597157.1; -.

13L; Z72930; CAA97159.1; -.

14; Z72930; S17019; S17019; S17019; S17019; S17019; S17019; S17019; S17019; S25321; S25221; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THIAZOLE. ALSO SEEMS TO HAVE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF01946; Thi4; 1.
AMS; TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; Mitochondrion; Transit peptide; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
326 AA;
                                                                                                                                                                                                                                        (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Praekelt U.M., de Oliveira R.C., Meacock P.A., Menck C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273:114-121(1997)
                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                          35,
40,
PubMed=8590279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 T
97 F
34991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.2%;
75.0%;
                                                                                                                                                                                            Last annotation
                                                                                                                                                                                                                 Last
                                                                                           Chroococcales; Synechocystis
                                                                                                                     PCC 6803)
                                                                                                                                                                                                                 sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIAZOLE BIOSYNTHETIC ENZYME FAD OR NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             843790F2CE00BF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROLE IN MITOCHONDRIAL
                                                                                                                                                                                                                                                                                        390 AA
                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caps
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RESULT
Y103_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                                                                                                                               MEDININE-9637999; pubMed-8680807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y103_METJA
Q57567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002460; MoCF_biosynth; 1.
TIGRRAMS; TICRN00177; molyb_syn; 1.
PROSITE; PS01079; MOCF_BIOSYNTHESIS_2; 1.
Molybdenum cofactor biosynthesis; Complete proteome SEQUENCE 390 AA; 43394 MW; 848183B5510CA314 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. 1. Sequence features in the 1 mb region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).

1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF A DEMOLYBDO-COFACTOR (MOLYBDOPTERIN), NECESSARY FOR MOLYBDO-ENZYMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-JAL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical MJ0103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00994; MOCF_biosynth; 1. Pfam; PF03453; MOEA_N; 1. Pfam; PF03454; MOEA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001453; MoCF_b:
InterPro; IPR005111; MoeA_C
InterPro; IPR005110; MoeA_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID~2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D64003; BAA10450.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European
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                                                                           -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Tanaka A., Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ь.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLVIPYEE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELXIPYEE 11
                                                          273:1058-1073(1996).
ILARITY: BELONGS TO THE UPF0063 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
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Bioinformatics Institute. There a
-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Last annotation protein MJ0103.
                                                                                                                                                                                                                                                                                                                                                                                                                                    / DSM 2661 / AFCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jannaschi i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35, last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MoeA_N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             848183B5610CA314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Best Local
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIW5_HUMAN
095279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 273:30863-30869(1998).
-I- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT LIGH EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                     Genew;
                                                                                    EMBL; AF084830; AAC79458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reyes R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99030343; PubMed=9812978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCNK5 OR TASK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome.
SEQUENCE 433 AA; 49866 MW; F82576531DF12142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U67467; AAB98083.1; -.
                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and expression of a novel pH-sensitive two pore domain channel from human kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01444; MoaA_NifB_PqqE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MJ0103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 EVEIPYEE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ELXIPYEE 11
                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KINEY, ALSO DETECTED
IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL
                                                                                                                                                                                                                                                                               ACIDIFICATION.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       K+ CONCENTRATIONS
                                                      603493;
                                                                     HGNC: 6280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
                  IPR003280;
IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000385; MoaA_NifB_PqqE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
K+channel_pore.
M+channel_nlg.
                                  K+channel_2pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.2%;
75.0%;
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Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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19;
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InterPro;

IPR000636;

InterPro; MEROPS; C04.005; EMBL; D00615;

1PR001730; Peptidase\_C4

JQ0494; JQ0494.

BAA00490.1;

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Query Match
Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Nuclear inclusion protein A (NI-A) (NIA)
(EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                use
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                Coat protein (CP)] (Fragme Ornithogalum mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00520; ion_trans; 1. PRINTS; PR01333; 2POREKCHANEL.
                                                           or send an
                                                                                                                                                                                                           -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECTIVIC
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                      Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; sskNA positive-strand viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                           also cleaved.
-i- CATALYTIC ACTIVITY: N oucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-12204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P20234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLG_OMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ELXIPYEE 11
                                                                                                                                                         PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
SIMILARITY: NI-A PROTEINASE BELONGS TO PROTIDASE FAMILY C4
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                        oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                                      {RNA}(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELSVPYEQ 485
                                                                                               non-profit
                                                         email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
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112
113
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1157
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215
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                                                                                             institutions as long as its content
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E871A7A4823DDA00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   µ₁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 499
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                                                                                                                                                                                                                                                                                                                                           STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Reidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Ilauna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Vonter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y928_METJA
Q58338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coat protein; Polyprotein.
Complete
                          TIGRFAMS; TIGR00537; hemK_rel_arch; 1.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                              REBASE; 4480;
                                                                                                                                                         EMBL; U67536;
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanococci; Meth Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MJ0928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, 15-JUL-1998 (Rel. 36, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
            Hypothetical protein; Transferase; Methyltransferase;
                                                        Pfam;
                                                                                  InterPro;
                                                                                                  InterPro;
                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MJ0928
                                                                      InterPro;
                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE HEMK FAMILY.
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PF00863; Peptidase_C4; 1.
plase; Transferase; Thiol protease; RNA-directed RNA polymerase;
                                       PF02475; Met_10; AMS; TIGR00537; h
                                                                                                                             MJ0928;
                                                                      IPR003402; Unk_Met10.
                                                                                 IPR004557; HemK_rel_arch IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001592; Poty_coat.
IPR001205; RNA_pol_P3D.
IPR001254; Ser_protease_Try.
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884
1136
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                                                                                                               M.MjaHemKP
                                                                                                                                                         AAB98930.1;
                                                                                                                                             IDUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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883
1136
                                                                                                                                                                                                                               rmatics Institute. There are no restrictions on institutions as long as its content is in no
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation update) (M.MjaHemkP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR INCLUSION PROTEIN COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1136;
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RESULT 15
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Best Local
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30-MAY-2000
15-JUN-2002
                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hahn F.M., Xuan J.W., Chambers A.F., Poulter C.D.; "Human isopenteny! diphosphate: dimethylally! diphosphate isomerase: overproduction, purification, and characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
       SEQUENCE
                                              Sterol biosynthesis; peroxisome; Magnesium.
ACT_SITE 86 86 RV CIMITADITAV
                                                                                                                                                                              EMBL; X17025;
                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 332:30-34(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96400329; PubMed-8806705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A human promyelocyte mRNA transiently induced by TPA is homologous to yeast IPP isomerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1sopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2)
1) (Isopentenyl pyrophosphate isomerase 1) (IPPI1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q13907
                                                                                           Propom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xuan J.W., Kowalski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-94292171; PubMed-8020941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                         Pfam; PF00293; NUDIX;
                                                                                                                     InterPro; IPR002667; InterPro; IPR000086;
                                                                                                                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jenomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                             (somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DII_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 ISARLKVPFEE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                              HOMOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP). CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                           INCLUDE BULLCHULS, VITAMINS A, B, E, AN CAROTEMOTUS HILE ACTUS AND CHOLESTEROL. SUBCEEDULAR EXCATION: PETOXISONAL.
                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE I FAMILY
                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: ISOPRENOID BIGSYNTHETIC PATHWAY WHOSE END PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate.
                                                                                                                                                    604055;
                                                                                                                                                               HGNC:5387; IDI1
                                                                                         PD004109; IPP_isomerase; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20:129-131(1994).
225
227
                                                                        Isoprene biosynthesis; Cholesterol biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
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                                                                                                                                                                              CAA34890.1; ALT_INIT.
      AA;
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39, Last sec
                  86
148
227
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      26319 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%;
45.5%;
                                                                                                                  NUDIX_hydrolase.
                                                                                                                                   IPP_isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chambers A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32;
Pred. No.
                 BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARGETING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2AE2377FE86EB217 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Denhardt D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                     AND K, STEROID HORMONES
                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 197
                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                      by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IPP isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Query Match 68.1%; Score 32; DB 1; Length 227;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSXELXIPYEE 11
| | | | | | | |
Db 112 LKAELGIPLEE 122

Search completed: January 15, 2003, 11:21:19
Job time: 11.2857 secs
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i A

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                              Score
  length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                           10:
11:
12:
13:
14:
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16:
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                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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76.6
74.5
774.5
774.5
772.3
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770.2
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770.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                                                                                                                               sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                         sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                        sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
                                                                                                                                                                                                                                                                                  sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                          sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                 sp_vertebrate:*
                                                                                                                                                                                                                                                                          sp_archeap:*
                                                                                                                                                                              Length
 1451
634
1028
1028
1028
274
291
381
738
233
233
461
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  16
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16
2 Q9YMM5
Q9XWY5
6 Q92FP6
6 Q8YAQ3
6 Q89F3
6 Q9Q4W5
1 Q9JK62
                                                                                1 Q9JMB8
1 P97528
Q94849
                                                                                                                Q9UQ52
                                                                                                                                                                              IJ
                                                                                                                          Q8U6Z1
Q9XI48
Q44755
                                                                        Q8RB89
                                                                                                                                                          066691
                                                                                                                                                                                                             SUMMARIES
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(without alignments)
88.635 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd.
                  Q8rb89 thermoanaer
Q9ymm5 lymantria d
Q9xwy5 caenorhabdi
Q9zfp6 listeria in
Q8yaq3 listeria mo
Q8yaq3 rhizobium l
                                                                               Q8u6z1 agrobacteri
Q9xi48 azabidopsis
Q44755 borrelia bu
Q9uq52 homo sapien
Q9jmb8 mus musculu
P97528 rattus norv
Q94849 drosophila
Q9q4w5
Q9jk62
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                                                                                                                                           066691 aquifex aeo
Q8u6z1 agrobacteri
           ornithogalu
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Q9РFJ3	Q9PUC3	Q8Y4X6	Q92FK3	049528	067512	Q24690	Q24363	Q8S9X6	Q8SVP8	030094	Q9V1T1	Q8TZZ4	Q9YA31	015268	Q93NQ2	Q9BQ74	Q8WUX8	Q961Z4	Q9NWW6	Q8U8F0	Q8Y3I4	092607	Q9ZQG2	094248	Q8REF7	Q8TJQ4	Q97YM6	059717
	brachydar		Q92fk3 listeria in		067512 aquifex aeo	Q24690 drosophila	irosoph	Q8s9x6 oryza sativ		030094 archaeoglob			aero			homo	homo		5		listeria		Q9zqq2 arabidopsis	chizosacch		Q8tjq4 methanosarc	97 ym6	O59717 schizosacch

## ALIGNMENTS

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RESULT 1
066691
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                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                  Pfam; PF00563; EAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
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066691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein AQ_367.
                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 850 AA; 97669 MW; C02DCEF91DBCDEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001633; EAL.
InterPro; IPR000160; GGDEF.
InterPro; IPR001993; Mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000686; AAC06656.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001993; Mitoch_carrier.
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                    80.9%;
54.5%;
3; Mismatches
                                                    Score 38; DB 16; Length 850; Pred. No. 15;
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            Indels
            0;
            Gaps
            0;
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QY

LSXELXIPYEE

1

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RESULT
Q9X148
ID Q9X
AC QS
DT 01
DT 01
DT 01
DT F9
GN F9
OC Eu
OC SE
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Q8U6Z1
ID Q8
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                                                                                                                                                                                                                                                  Q9XI48;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                             F9L1.15 protein. F9L1.15.
                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the plant pathogen and Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001) EMBL; AE009395; AAL45459.1; ALT_INIT. EMBL; AE008220; AAK88782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cielo C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21608551; PubMed=11743194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608550; PubMed=11743193;
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                                                                                                                                                                                                                                                                                                                                                                                                                         200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                      LAHDLDIPYEE 210
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ISREMDVPYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Slater S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 AA;
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53483 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%;
63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16C1085B5A12B21B CRC64;
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                                                                                                                                                                 update)
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Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                               core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
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                                                      Tracheophyta;
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. Jr., Woo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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N

SXELXIPYEE 11

Conservative

Ν.

2;

Indels

0;

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0;

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RESULT 4
Q44755

ID Q44755

ID Q4475

ID Q447

Q447

D7 01-N

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D7 01-N

D8 BB0

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Best Local S
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Best Local
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                             Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathiqra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q44755
Q44755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interro, annough Pfam; Pfam; Pfam; Pfondon; ABC_transportr; 1.
Probom; PD000006; ABC_transportr; 1.
SMART: SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; Dunn J.J., Butler-Loffre Submitted (DEC-1995) to
                                                                                              Complete proteome. SEQUENCE 634 AA;
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STRAIN-ATCC 35210 / B31;
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"Arabidopsis thaliana chromosome 1 BAC F9L1 sequence.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AC007591; AAD39650.1;
                                                                                                                                                 TIGR; BB0267; -
                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                    Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98065943; PubMed-9403685;
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Bacteria; Spirochaeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB0267
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ATP-binding.
1451 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=139;
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InterPro; IPR003439; ABC_transportr.
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                                                                                                                                                                                               U43739; AAA85591.1;
                                                                                                                                                                U43739; AAA85591.1; -. AE001137; AAC66681.1;
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  Similarity 6; Conser
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                                                                                                 70752 MW;
                      74.5%;
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54.5%;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , WM
                         Score 35;
Pred. No.
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                                                                                              E8AFB112B121F3B8 CRC64;
ed. No. 48;
Mismatches
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                                        Length 634;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                    Q9JMB8;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
O1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DCT-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                           "Expression and regulation of a gene encoding neural recognition molecule NB-3 of the contactin/F3 subgroup in mouse brain."; Gene 245:253-266(2000).
                                                                                                                    SEQUENCE FROM N.A.
STRAIN=129SVJ; TISSUE-BRAIN;
MEDLINE=20183687; PubMed=10717476;
Lee S., Takeda Y., Kawano H., Hosoya H.,
Takahashi N., Watanabe K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 4. Pfam; PF00047; ig; 6. SMART; SM00060; EN3; 3. SMART; SM00408; IGC2; 5. SMART; SM00410; IG_like; 1. PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                            EMBL; AB032602; BAA92367.1;
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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MEDLINE-98146168; PubMed=9486763;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNB-3
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les 6; Conserv
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P20241; 1CFB.
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AB003592; BAA82612.1; -.
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IPR003600;
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IPR003961; FN_III.
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Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35;
Pred. No. 8
2; Mismatch
                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                              Nomoto M.,
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                                                                                                                                              Fujimoto D.,
                                                                                                                                                                                                                                                                                                 Murinae; Mus
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RESULT 8 Q94849 ID Q948

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Pfam; PF00047; lq; 6.
SMART; SM00060; FN3; 4.
SMART; SM00408; IGC2; 5.
SMART; SM00410; IG_like; 1.
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01-MAY-1997
                                                                                                                                                                                                                                                           MEDLINE-97101230; PubMed-8945756;
Ogawa J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.;
"Novel neural adhesion molecules in the Contactin/F3 subgroup of the immunoglobulin superfamily: Isolation and characterization of cDNAs from rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; 1PR003600; Ig_like.
InterPro; IPR003006; Ig_Hike.
Pfam; PF000411: '__
                                                                                                                                                                           InterPro; IPR003600; Ig_lik
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=WISTAR; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Immunoglobulin domain.
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SMART; SM00408; IGC2; 5.
SMART; SM00410; IG_like; 1.
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                                                                                       SEQUENCE
                                                                                                                                                                                                       InterPro; IPR003598;
                                                                                                                                                                                                               InterPro; IPR003439; ABC_transportr.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                    Neurosci
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P97528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003439; ABC_transportr.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD;
                                                                                                              PROSITE;
                                                                                                                                                                                                                                        EMBL; D87248; HAA13320.1;
                                                                                                 [mmunoglobulin domain
 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                959 SAELLVPFEE 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 6; Conserv
                     2 SXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SXELXIPYEE 11
SAELLVPFEE 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1858223; Cntn6
                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                . Lett. 218:173-176(1996).
                                                                                                            PS00211;
                                                                                                                                                                                                                                                                                                                                                                                                          7 (TrEMBLrel.
7 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                      1028 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 AA;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                          ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                               Rodentia;
                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                    74.5%;
60.0%;
                                                                                                                                                                                         Ig_c2.
lg_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113759 MW;
                                                                                      114065 MW;
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19,
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Last annotation update)
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                                                    Score 35; DB
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                      47EFD8A370CF4923 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHEC59F86CA3978F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 AA
                                                              DB 11; Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 1028;
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                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                            MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong S., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; (
Thermoanaerobacteriales; Thermoanaerobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila buzzatii (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila inferred from a molecular phylogeny."; Curr. Biol. 5:1129-1139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96120851;
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                           Transferase;
                                                                                                                                                                                                                                                                                 Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyase.
ILVE OR TTE0933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8RB89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8RB89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0016167; Dbuz\Yp1.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U52126; AAC47249.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Pattern of ecological shifts in the diversification of Hawaiian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kambysellis M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q94849;
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 LISELELPYE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSXELXIPYE 10
                                  1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                 e Res. 12:689-700(2002).
AE013059; AAM24189.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00151; lipase;
                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
6; Conserv
                                                                                                              Similarity
                                                                                                                                                                                                 291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 AA;
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                           Aminotransferase; Complete proteome. 91 AA; 32346 MW; 105072D27AB06FFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HO K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8548285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30637 MW;
                                                                                                              72.3%;
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                                                                                     Score 34;
Pred. No.
3; Mismato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772CFE9AE771BB48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                        Mismatches
                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
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33;
                                                                                                                 35;
                                                                                                                                     g BB
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                                                                                                                                        Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridia;
; Thermoanaerobacter.
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                                                                                                                                                                                                                                                                                                                                                           Υ.,
                                                                                                                                                                                                                                                                                                                                                                                       Yang
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                                                                                     Caps
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RESULT 11

Q9XWY5

ID Q9XWY

AC Q9XWY

AC Q9XWY

AC Q9XWY

DT 01-V

DT 01-V

DT 01-V

DT 01-V

DT 01-V

ROS Caer

OC Rhuki

OC Rhuki

OC Rhuki

CRA Mai

RN [2]

RP SEC

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RA Wij

RA G

R
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Q9YMM5
ID Q9YMM
AC Q9YMM
DT 01-MA
DT 01-DE
DE LJOORF
OS Lyman
OC Lyman
OC Nucle
OX NCBL
RN [1]
RN [1]
RA KUZIC
RT Lyman
RL Lyman
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Best Local
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                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighting J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LdOrf-102 peptide.
Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMSLIE) 12,
01-NOV-1999 (TERMBLIE) 12,
01-JUN-2001 (TERMBLIE) 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XWY5;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuzio J., Pearson M.N.,
Slavicek J.M., Rohrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9YMM5
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y66A7A.5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar."; Virology 253:17-34(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99124785; PubMed-9887315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=10449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y66A7A.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ELDLPYEE
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G.F.;
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Pred. No.
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RA Charbit A., Chetouani F., Couve B., de Daruvar A., Dohoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusboux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusboux P.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurarkat G.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurarkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nudjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Doland J.-A., Voss H., Webland J., Cossart P.:
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
RE FIGURE CONTRACT 
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       Q8YAQ3
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STRAIN=CLIP 11262 / SEROVAR 6A;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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PROSITE; PS50071; HOMEOBOX_2; 2.
SEQUENCE 738 AA; 87325 MW; FAA0174853A0E2A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:2012-2018(1998).
EMBL; AL032622; CAA21499.1; -.
EMBL; AL590342; CAC35859.1; -.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11679669;
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nes 7; Conserv
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33 AA; 27625 MW; E1E405DC3C6048EB CRC64;
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                                                                                                                                                                                                                                                                                                                               0;
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0; Mismatches
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       PRT;
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       233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 233;
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                                                                                                                                                                                                                                                                      Kaneko "., Nakamura Y., Sato S., Asamizu H., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kohara M., Nakayama S., Nakazaki N., Shimpo S., Sugimolo M.,
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Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Bonder A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                               MEDITINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Messorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative genomics of Listeria species.";
Science 294:849-852(2001).
EMBL: AL591973; CAC98279.1; -.
Probom; PD006892; GH_4; 1.
PROSITE; PS01324; GLYCOSYL_HYDROL_F4; UNKNOWN_1.
                                                           Pfam; PF02056; Glyco_hydro_4; 1. PRINTS; PR00732; GLHYDRLASE4.
                                                                                                                                          EMBL; AP003009; BAB52744.1; -.
                                                                                                                                                                                                "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                     Takeuchi C., Yamada M., Tabata S.;
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01-00N 2002 (Tribbing rel
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                                                                                                                InterPro; IPR001088; GH_4.
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7; Conserv
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63.68;
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21, Last annotation updat
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20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18, Created)
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Pred. No. 45;
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RESULT 15
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AC Q9Q4W
DT 01-MA
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Search completed: January 15, 2003, 12:35:38 Job time: 35.5714 secs
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Best Local Simi arity
Matches 6; Conserv
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G9Q4W5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Polyprotein (Fragment).
Ornithogalum mosaic virus.
Ornithogalum mosaic virus.
Ornithogalum mosaic virus.
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SEQUENCE FROM N.A.

"Potyviruses in Australia.";

"Potyviruses in Australia.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF203528; AAF22752.1; -.

InterPro; IPR001592; Poty_coat.

InterPro; IPR001205; RNA_pol_PJD.

pfam; PF00767; Poty_coat;

InterPro; IPR001205; RNA_pol_PJD.

pfam; PF007680; RNA_dep_RNA_pol; 1.

Pfam; PF00680; RNA_dep_RNA_pol; 1.
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NCBI_TaxID=12204;
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27 KLSIPYEE 34
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                                                                                                                                                                                                                                                                                                                               70.2%; Score 33; DB 12; Length 465; 75.0%; Pred. No. 93; tive 1; Mismatches 1; Indels
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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47
1 LSXELXIPYEE 11
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
 BLOSUM62
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em_htgo_other:*	em htgo mus:*	em_htgo_hum:*	em_sy:*	em_htg_vrt:*	em_htg_mam:*	em_htg_rod:*	em_htg_pln:*	em_htg_mus:*	em_htq_other:*	em_htg_inv:*	em_htg_hum:*	em_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

## O No. Score Match Length DB AR063636 AR086117 AR089547 I15437 AR023961 AR054698 AR112315 AR112316 AX093143 AX093145 AX317584 AX317576 AX317576 AX317576 AX317578 AX317578 AR093638 AR193577 AR206175 AR206169 AX317151 AR093632 AR193571 AX404966 AX404972 AR063642 AR086123 AR061700 AR061941 AR061694 AR061935 138585 176140 AX317586 AR023936 AR089553 AR054704 AR023967 AF315118 IJ 124097 AR112315 Sequence AR112316 Sequence AX093143 Sequence AX093145 Sequence AX317584 Sequence AX317568 Sequence AX317576 Sequence AX317576 Sequence AX317578 Sequence AX404968 Sequence AX404968 Sequence AR023967 Sequence AR054704 Sequence AR061941 Sequence AR061941 Sequence AR063642 Sequence AR063642 Sequence AR08553 Sequence AR089553 Sequence AR093638 Sequence AR093638 Sequence AR0936375 Sequence AK023936 Sequence AX317586 Sequence I15437 Sequence 5 AR093632 AR193571 AR063636 AR086117 AR2061 AX3171 AR054698 Sequence AR061694 Sequence 124097 Sequence 12 138585 Sequence 12 176140 Sequence 12 AR023961 Sequence Description 124091 AF315118 Sequence Populus

RESULT 1

ALIGNMENTS

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                                                                                                                                                                                                                                                               Sequence 12 from patent AR023967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-OCT-2000) Biology, Tsinghua East Rd. No.35, Beijing Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1079)
Huiming, Z. and Xin, S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus euphratica clone PSR1 salt-induced mRNA sequence.
AF315118
                                                                                                                                                                                           Unclassified.
                                                                                                                                                                                                          Unknown
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/dev_stage="two years old"
/note="isolated using suppression subtractive
hybridization of uninduced vs. salt-induced root tips;
cloned using RACE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Populus euphratica"
/db_xref="taxon:75702"
/clone="PSR1"
                                                                               /organism="unknown"
519 c 553 g
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AR061700
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                                                        Alignment Scores: Pred. No.:
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Sequence
AR054704
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Sequence
AR061700
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Heisler,L.M., Fors,L. and Brow,M.Ann.D.
Rapid detection of mutations in the p53 gene
Patent: US 5843654-A 12 01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: US 5837450-A 12 17-NOV-1998;
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Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann.D.
Detection of target nucleic acid molecules using thermostable
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US-09-823-649A-2 (1-11) x AR061700 (1-1600)

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BASE COUNT
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Raiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-I endonucleases
Patent: US 5843669-A 12 01-DEC-1998;
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Brow,M.Ann.D., Hall,J.Steven.Grotelueschen., Lyamichev,V.,
Olive,D.Michael. and Prudent,J.Robert.
Detection of nucleic acid sequences by invader-directed cleavage
Patent: US 5846717-A 12 08-DEC-1998;
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RESULT 7
AR086123
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AR086123
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                                                                                                                                                                                                                                                                                                       Unknown
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Dahlberg,J.E.
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RESULT 11
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Prudent, J.R., Hall, J.G., Lyamichev, V.I.,
pahlberg, J.E.
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  AR206175
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Sequence 12 from patent US 6348314.
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I38585
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AR206175
AR206175.1 GI:21504699
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Dahlberg,J.E., Lyamichev,V.I. and Brow,M.Ann.D.
Nucleic acid encoding synthesis-deficient thermostable DNA
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Dahlberg, J.E., Lyam.Chev, V.I. and Brow, M.Ann.D.
Detection of target nucleic acid molecules using
synthesis-deficient thermostable DNA polymerase
Patent: US 5691142-A 12 25-NOV-1997;
Location/Qualifiers
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Dahlberg,J.E., Lyamichev,V.I. and Brow,M.Ann.D.
5' nucleases derived from thermostable DNA polymerase
Patent: US 5614402-A 12 25-MAR-1997;
1 (bases 1 to 1682)
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Thermostable polymerase
Patent: US 6130045-A 1 10-OCT-2000;
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190.345 Million cell updates/sec
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1. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

4. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5. /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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11:
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5. //SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
7. /SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
8. /SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
9. /SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
9. /SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
10. /SIDS2/gcgdata/genesed/geneseqn-embl/NA198.DAT:*
11. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
12. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
13. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
14. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
15. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
16. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
17. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
18. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
20. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
21. /SIDS2/gcgdata/genesed/geneseqn-embl/NA199.DAT:*
22. /SIDS2/gcgdata/genesed/geneseqn-embl/NA2000.DAT:*
23. /SIDS2/gcgdata/genesed/geneseqn-embl/NA2001.DAT:*
23. /SIDS2/gcgdata/genesed/geneseqn-embl/NA2001.DAT:*
23. /SIDS2/gcgdata/genesed/geneseqn-embl/NA2001.DAT:*
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Ygapext
Fgapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

22-DEC-1994

W09429482-A.

RESULT 1
AAQ80745
ID AAQ80
XX AAQ8
AC AAQ8
AC AAQ8
XX DNAXX DNAXX

5' Nuclease from Tag DNAP

DNA-polymerase; DNAP; Taq; DNA cleavage; RNA cleavage; 5' nuclease; ds.

19-JUL-1995 (first entry)

AAQ80745;

AAQ80745 standard; DNA; 1600 BP.

ALIGNMENTS

Thermus aquaticus YT-1

45	44	43	42	41	40	<b>2</b> 9	38	37	<b>3</b> 6	35	34	33	32	<b>ω</b>	30	29	28	27	26	25	24	23	22	21	20	19	18	17		15	14	<u>ا</u> لا ا	. C. L.	10	. 6	œ	7	6	51	4	ω	2		Result
44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44		44	44			4.	44	44	44	44	44	44	44	44	44	44	44		Score
93.6	93.6	93.6		93.6	ω,	ω ·	$\omega$	·	w ·	ω	w •	ω.	w	ω.	w	ω.		ω.	ω.	ω.	w	93.6	w •	ω	w	ω.		Ψ	·	w.	w i	، س	02. 00.	ب د	·	Ψ	ω.	ψ.	93.6	ū.	ů.	w ·	93.6	Query
2496	2496	2493	2370	2370	2367	2364	2277	2277	2277	2274	2043	2043	2043	2043	1965	1904	1899	1899	1899	1899	1896	1812	1812	1794	79	1696	1689	1689	1686	1686	1686	1686	1683	1635	1635	1635	1600	1600	1600	1600	1600	1600	1600	Length
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AAV65780	AAQ80750	AAQ24005	AAQ24324	AAQ24012	AAQ24006	AAQ23995	AAQ24325	AAQ24007	AAQ24013	AAQ23994	AAQ24326	AAQ24320	AAQ23996	AAQ24008	AAD24823	AAD24822	AAD24819	AA024327	AAQ24321	AAQ24009	AAQ23997	AAS00718	071	AAT27255	AAT32327	AAZ29461	AAX27131	AAT47960	AAX27132	AAX27130	AAT47961	AAT47959	AAQ24328	AAQ24322	AAQ23998	AAQ24010	AAV63407	AAV53855	AAV65786	AAT76647	34	768	AAQ80745	ΩI
	<	Mulant thermostabl	Mutant thermostabl	4		ŗ	~+	~		thermostab	thermostab	thermostab	_		(PL) -		0				hermosta		meric CauTaq D	ymerase	Thermus flavus DNA	Thermostable DNA d		Ω.	polymerase	lymer		Mutant Tag polymer	Thermostable DNA d		Mutant thermostabl	Mutant thermostabl	DNA sequence of a	Nucleotide sequenc	Thermus aquaticus	U I	Synthesis deficien	mus ao	Nuclea	Description

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AAT27686

AAT27687

XX

XX

AAT27

XX

AAT27

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AAT27

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AAT27

AAT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Taq DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/selection protocol was used to isolate clone 4B containing a mutated Taq DNAP gene (mutTag) (sequence given in AAQ80746) having normal 5' nuclease activity but less than 18 of the wt Taq DNAP activity. mutTaq was cut from pTTQ18 by EcoRI-SalI digestion and cloned into pET-3c. Thus clone was digested with BstXI and BamHI. The DNA was treated with DNAPECI Klenow fragment and dNTPs, blunt-ended and religated, resulting in an in-frame deletion of 903 nucleotides. The DNA sequence of the resulting 5' nuclease is given in AAQ80745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
No.:
                                                                                                                                                                                                                                                                                                                                                                                           p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shi Staphylococcus; identification; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
30-AUG-1995;
09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 95-96; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1993;
                                                                       09-NOV-1995;
                                                                                                                        23-MAY-1996
                                                                                                                                                                      W09615267-A1
                                                                                                                                                                                                                                                                                                                                             Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT27686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-036504/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT27686 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9305-0073384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aquaticus DNA polymerase coding sequence (Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US06253
  94US-0337164
                         95US-0520946
                                                                       95WO-US14673
                                                                                                                                                                                                                                                                     Location/Qualifiers 14..1600
                                                                                                                                                                                                                    /product= Mutant DNA polymerase
                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44,00 * 81.82* 81.82* 93.62*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 G; 242 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium; Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
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B Qγ

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Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the vector was digested with BSTXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPECI to trim both 3' the both and the property of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1995;
07-JUN-1995;
overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. The resulting mutant Tag polymerase is also referred to as the Cleavase BB enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage of nucleic acids to detect esp. in human p53 gene, to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oldenburg MC, Olive
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95US-0484956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heisler LM,
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strains of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyamichev VI;
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Alignment Scores: Pred. No.: Best Local Similarity: Percent Similarity 44.00 81.82% 81.82% 93.62% 1.89 Length: Matches: Mismatches: Conservative:

Indels: Gaps:

Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;

US-09-823-649A-2 (1-11) x AAT27686 (1-1600)

1133 **ب** CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165 LeuSer\*\*\*GluLeu\*\*\*IleProTyrGluGlu 11

RESULT 3 AAT70347 AAT70347 standard; DNA; 1600

03-APR-1998 (first entry)

AAT70347;

Synthesis deficient Taq DNA polymerase gene clone 4F.

DNA polymerase; taq polymerase gene; DNAP; 5' nuclease activity; Cleavase BB; DNA cleavage; reduced synthetic activity; ss.

Thermus aquaticus Synthetic

Y PART OF THE PROPERTY OF THE

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RESULT 4
AAT76647
ID AAT7
XX AAT7
XX AAT7
XX Taq
DT 14-A
XX Taq
DX Taq
XX Taq
XX Taq
XX Top
XX Synt
XX Synt
XX Synt
XX Sol
PN W097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-823-649A-2 (1-11) x AAT70347 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment
                   02-DEC-1996;
24-JAN-1996;
12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence, clone 4F, encodes a Taq DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mutTaq construct described in AAT70343. The entire mutTaq gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BstXI and BamHJ, at unique sites. The 3' overhang of BstXI was trimmed to a blunt end, while the 5' overhang of BamHI was filled in. The blunt ends were ligated together. This resulted in an in-frame deletion of 903 nucleotides. The enzyme
                                                                                                                                                                                                         Thermus aquaticus YT-1. Synthetic.
                                                                                                                                                                                                                                                        Nucleic acid cleavage; DNA cleavage; RNA cleavage; Taq; DNA polymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                                                                                            Taq gene 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1600 BP; 286 A; 519 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2A; Columns 79-82; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-201481/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5614402-A
   02-DEC-1996;
                                                                                                        22-JAN-1997
                                                                                                                                        31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                  AAT76647;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT76647 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded by the present protein is also referred to as Cleavase BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                        WO9727214-AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahlberg JE,
                                                                                                                                                                                                                                                                                                              nuclease clone 3F (Cleavase BB).
                                                                                                                                                                                                                                                                                                                                                (first entry)
                   96US-0759038.
96US-0599491.
96US-0682853.
96US-0756386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0986330.
93US-0073384.
                                                                                                        97WO-US01072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0254359
   96US-0758314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                                                                                                                                                                                                                                               nuclease;
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  material for the construct. Cleavase BB is a thermostable structure-specific nuclease preferred for use in nucleic acid cleavage methods of the invention. Mutant genes (AAT76644-47) were constructed in order to determine which portions of the Tag polymerase domain can be altered without eliminating 5' nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA. It relates to methods for forming a NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' nuclease activity of various enzymes (see AAW24210-13) is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific NA sequence or specific variations of them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      altered Thermus aquaticus DNA polymerase (Taq) gene in which nucleotides 875-1778 of the wild-type gene coding sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-393613/36
                                                                                                                                                                       Thermus aquaticus strain YT-1. Synthetic.
                                                                                                                                                                                                                                         Nucleic acid detection; multiple sequential invasive cleavage;
                                                                                                                                                                                                                                                                          Thermus aquaticus nuclease clone 3F (Cleavase BB) DNA
                                                                                                                                                                                                                                                                                                              02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   characterisation of nucleic acid (NA) sequences and variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence, denoted clone 3F or Cleavase BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 245; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterisation of nucleic acid sequences and variations in nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable structure-specific nuclease(s) - used for detection and
   (THIR-) THIRD WAVE TECHNOLOGIES INC
                                     24-MAR-1997;
                                                                    24-MAR-1998;
                                                                                                        01-OCT-1998
                                                                                                                                        W09842873-A1
                                                                                                                                                                                                                         DNA polymerase; nuclease; Cleavase BB; ds
                                                                                                                                                                                                                                                                                                                                                AAV65786;
                                                                                                                                                                                                                                                                                                                                                                                  AAV65786 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuSer***GluLeu***IleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant gene mutTaq (see AAT76643) was used as the starting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to means for the detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahlberg JE, Prudent JR;
                                                                                                                                                                                                                                                                                                              (first entry)
                                     97US-0823516
                                                                    98WO-US05809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.00
81.82%
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93.62%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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                                                                                                                                                                                                                                                                                                                                                                                  ğμ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises an
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AC AAV'
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DE Nuc.
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XW Cloi
XW mut.
XW hepp
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YX
PF 26-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus (Taq). In comparison to the wild-type Taq DNAP sequence (see AAV65779), it contains an in-frame deletion of 903 nucleotides. The invention relates to means for the detection and characterisation of nucleic acid sequences, and variations in nucleic acid sequences. It also relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving this structure in a site-specific manner, preferably using a thermostable structure-specific nuclease such as a modified Tag that that has reduced synthetic activity (see AAV65783-86). Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brow MAD,
Mast AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific nucleic acid sequences or specific variants. The invently further relates to methods for the separation of nucleic acid molecules based on charge, methods for the detection of non-target cleavage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic protein binding region, and methods for the detection of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential amplification processes, and allows many targets to be analysed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                                                                                                                                                                                                                                                                                                                                                                                                         1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a single reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleotide sequence (clone 3F) codes for a thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 278; 524pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-557036/47
                  26-NOV-1997;
                                                     04-JUN-1998
                                                                                      WO9823774-A1
                                                                                                                         Thermus sp.
                                                                                                                                                          mutant DNA polymerase; bacteria; fungi; protozoa; RNA virus; hepatitis C virus; HCV; ds.
                                                                                                                                                                                           Clone 4D; Tag mutant gene; thermostable; structure-specific nuclease;
                                                                                                                                                                                                                                Nucleotide sequence
                                                                                                                                                                                                                                                                   21-DEC-1998
                                                                                                                                                                                                                                                                                                    AAV53855;
                                                                                                                                                                                                                                                                                                                                     AAV53855 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the cleavage structure by the nuclease indicates the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclease (Cleavase BB) derived from the DNA polymerase (DNAP) of
                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuSer***GluLeu***IleProTy:GluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Hall JG,
Vavra SH;
                                                                                                                                                                                                                                                               (first entry)
                    97WO-US21783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.89
44.00
81.82%
81.82%
93.62%
                                                                                                                                                                                                                                of clone 4F of the Tag gene mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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RESULT 7
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                AAV63407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                        1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of a clone of a mutant Taq gene, used in the method of the invention. In this process thermostable structure-specific nucleases are derived from mutant DNA polymerases, which can be used for detecting mutant alleles or strains of microorganisms. The structure-specific nucleases can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mixtures, compositions and kits to treat nucleic acid, e.g. for detection of wild type and mutant alleles of genes, for detection and/or identification of strains of microorganisms such as bacteria, fungi, protozoa, especially for detection of RNA viruses such as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1600 BP; 286 A; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable structure-specific nuclease(s) derived from mutant DNA polymerase(s) - useful for detecting mutant allele(s) or strains of
 Brow MAD,
                                                     06-JUN-1995;
                                                                  07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                            Thermostable DNA polymerase; nucleic acid detection; Cleavase BB thermostable 5' nuclease; ds.
                                                                                                                                                                                                                                                                                    DNA sequence of a thermostable 5' nuclease derived from Taq polymerase.
                                                                                                                                                                                                                                                                                                               26 JAN 1999
                                                                                                                                                                                                                                                                                                                                          AAV63407;
                                                                                                                                                                                                                                                                                                                                                                   AAV63407 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatitis C virus (HCV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                            06-JUN-1994;
                                                                                                                        06-JUN-1995;
                                                                                                                                                 17-NOV-1998
                                                                                                                                                                            US5837450-A
                                                                                                                                                                                                     Thermus aquaticus
                          (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       MM
Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyamichev VI,
                                                                                                                                                                                                                                                                                                             (tirst entry)
                                                   92US-0986330.
93US-0073384.
95US-0471066.
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96US-0757653.
                                                                                            94US-0254359
                                                                                                                       95US-0471066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.89
44.00
81.82*
81.82*
93.62*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indels:
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US-09-823-649A-2 (1-11) x AAV63407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the presence of a nucleic acid molecule. The method is used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     where the 5' nuclease is capable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The nuclease, designated Cleavase BB, is used in a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a thermostable 5^\prime nuclease derived from a thermostable polymerase modified to have reduced synthetic activity,
                                                                                                                                                                                                                                                                                        old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Mutant thermostable DNA polymerase pSPSA288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These can be used in
                    Abramson RD,
                                                                                                                                                 30-SEP-1991;
                                                                                                                                                                               16-APR-1992
                                                                                                                                                                                                             WO9206200-A
                                                                                                                                                                                                                                                                                                                                      Thermus species sps17
                                                                                                                                                                                                                                                                                                                                                                        5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ24010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ24010 standard; DNA; 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Columns 79-82; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-023438/02
                                                  (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSer***GluLeu***IleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        forensic testing or paternity determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) BP;
                    Gelfand DH;
                                                                              90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                 91WO-US07035
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                                                                                                                                                                                                                                                                            /*tag=
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                                                                                                                                                                                                                                           "nucleotides 4-861 deleted from the native sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase enzyme produced to exhibit a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCN, self-sustained sequence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                               28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-150885/18.
P-PSDB; AAR23157.
                                                                                                                                                                                                                                                                                                                         5'-3'; exonuclease;
                                                                                                                                                                                                                                                                                                                                                    Mutant thermostable DNA polymerase pLSC8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ23998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 59; 185pp; English.
(CETU ) CETUS CORP
                                                                                                30-SEP-1991;
                                                                                                                                16-APR-1992.
                                                                                                                                                            W09206200-A.
                                                                                                                                                                                                                                           old_sequence
                                                                                                                                                                                                                                                                                         Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ23998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1635 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     has been mutated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is that of Thermus species sps17 polymerase DNA which been mutated. The mutation designated pSPSdA288 causes the vmerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCCCAGGAGCTCTCCATCCCCTACCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                               90US-0590213.
90US-0590466.
90US-0590490.
                                                                                               91WO-US07035
                                                                                                                                                                                                           /note= "nucleotides 4-867 deleted from native
                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      PCR; amplification; SSR; sequencing; PLCR; ss
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                                                                                                                                                                                         sequence"
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                       1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
 28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                             5'-3';
                                                                                                                                                                                                                                                                        Mutant thermostable DNA polymerase pZ05A292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
                                         30-SEP-1991;
                                                                                                 WO9206200-A
                                                                                                                                                                       old_sequence
                                                                                                                                                                                                                Thermus species Z05.
                                                                                                                                                                                                                                                                                                       22-OCT-1992
                                                                                                                                                                                                                                                                                                                                  AAQ24322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1635 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ23993-Q24013,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            been mutated. The mutation, resulting in the polymerase enzyme produced to exhibit
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                                                                     16-APR-1992
                                                                                                                                                                                                                                                                                                                                                               AAQ24322 standard; DNA; 1635 BP
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                                                                                                                                                                                                                                           exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                                                                                     (first entry)
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90US-0590466
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                                                                                                                            "nucleotides 4-873 deleted from the native sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 G; 246 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant pLSG8, causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase DNA which has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1168 CTCTCCCAGGAGCTTGCCCATCCCCTACGAGGAG 1200
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See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                      Key
old_sequence
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                                                       16-APR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant thermostable DNA polymerase pTTHA292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1635
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                                                                                                                                                                                                                                                                                                                                             Thermus
                                                                                                                                                                                                                                                                                                                                                                                              5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
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                                                                                                                                                                                                                                                                                                                                             thermophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of Thermus thermophilus polymerase DNA which has been mutated. The mutation designated pTHAR292 causes the polymerase enzyme produced to exhibit a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                    Thermostable DNA dependent polymerase; nuclease activity; Taq polymerase; mutant; Polymerase Chain Reaction; PCR, N-terminal domain; proteolytic; thermal stability, hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer-driven mutagenesis; identification of pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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                                                                                      Synthetic.
                                                                                                          Thermus aquaticus
                                                                                                                                                    mutational analysis; forensic identification; ds.
                                                                                                                                                                                                                                                                              Thermostable DNA dependent mutant Taq polymerase-1 encoding DNA
                                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                  AAZ29460;
                                                                                                                                                                                                                                                                                                                                                                                                          AAZ29460 standard; DNA; 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1635 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCCCAGGAGCTTGCCATCCCCTACGAGGAG 1200
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                                                                                                                                                                                                                                                                                                                        (first entry)
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90US-0590466.
90US-0590490.
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                                            Location/Qualifiers
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81.82%
81.82%
93.62%
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                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
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    30-MAY-1996;
                                                04-DEC-1996.
                                                                                        EP745676-A1
                                                                                                                                                                                                                                      Mutant Taq polymerase FY2.
                                                                                                                                                                                                                                                                                   11-MAY-1997
                                                                                                                                                                                                                                                                                                                          AAT47959;
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WPI; 2000-105869/09.
P-PSDB; AAY44352
                                                                            Wurst H, Qui Z;
                                                                                                                           (CLON-) CLONTECH LAB INC
                                                                                                                                                                           98US-0096399
                                                                                                                                                                                                                             99WO-US13305.
                                                                                                                                                                                                                                                                                                                                                                                /product= "Thermostable mutant Tag polymerase-1" /note= "Identical at C-terminus to Tag polymerase from Thermus aquaticus"
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Novel enzyme, particularly useful in polymerase chain reaction

dependent, mutant Tag polymerase-1 enzyme. The N-terminal domain of the polymerase includes a sequence of 9 amino acids, that has 40.50% sequence identity with residues 280-288 of native Thermus aquaticus polymerase, Tag. The residues 10.553 of encoded by this sequence is identical to residues 289-832 of Tag polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) based processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, densities of the contraction of the cont The present sequence is the DNA encoding a novel, thermostable DNA ldentification of pathogens, mutational analysis and forensic

Sequence 1682 BP; 286 A; 567 C; 575 G; 254 T; 0 other;

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US-09-823-649A-2 (1-11) x AAZ29460 (1-1682)
                                                                                           Best Local Similarity:
                                                                                                       Percent Similarity:
1202 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1234
             1 LeuSer***GluLeu***1leProTyrCluGlu 11
                                                                     44.00
81.82%
81.82%
93.62%
                                                                 Gaps:
                                                                                          Conservative: Mismatches:
                                                                                Indels:
                                                                                                                  Matches:
                                                                                                                             Length:
                                                                     1682
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AAT47959 standard; DNA; 1686 BP

(first entry)

DNA sequencing; PCR; polymerase; FY2; FY3; FY4; thermostable; SS. Thermus;

Thermus aquaticus

96EP-0303880

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RESULT 14
AAT47961
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FY2, FY3 and FY4 (see AAT47959 to AAT47961) are new thermostable DNA polymerases providing improved results in DNA sequencing reactions. FY2 is the T. aquaticus DNA polymerase lacking pref. the 271-272 N-terminal amino acids and having the amino acid at position 667 of the wild type (Phe) replaced by Tyr. FY3 contains 562 amino acids with a Met at position 1 and Ala at position 2, corresponding to the Met and Ala of positions 271 and 272, respectively, of the wild type enzyme. FY4 corresponds to the T. thermophilus DNA polymerase lacking the N-terminal 274 amino acids having a Phe to Tyr replacement at position 396 (position 669 of the wild type enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 10-13; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase and lacking 5' to 3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW09315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis
                                                                                                                                                                                                           Mutant Taq polymerase FY4.
                                                                                                                                                                                                                                                                                                              1219 CICTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1995;
       P-PSDB; AAW09317
                                    Davis M,
                                                                                              30-MAY-1996;
                                                                                                                                        EP745676-A1
                                                                                                                                                         Thermus thermophilus
                                                                                                                                                                                                                                                                       AAT47961 standard; DNA; 1686 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1686
                WPI; 1997-013699/02
                                                       (AMSH ) AMERSHAM LIFE SCI INC.
                                                                           31-MAY-1995;
                                                                                                                   04-DEC-1996
                                                                                                                                                                               DNA sequencing;
                                                                                                                                                                                                                              11-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           No
                                                                                                                                                                                                                                                                                                                                 1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                       polymerase;
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                                    Fuller C,
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                                                                           95US-0455686
                                                                                              96EP-0303880
                                                                                                                                                                              PCR; s
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                                                                                                                                                                                        FY3; FY4; thermostable; Thermus; enzyme;
                                     B
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                                     Fuller
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Indels:
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US-09-823-649A-2 (1-11) x AAT47961 (1-1686)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerases providing improved results in DNA sequencing reactions. FY2 is the T. aquaticus DNA polymerase lacking pref. the 271-272 N-terminal amino acids and having the amino acid at position 667 of the wild type (Phe) replaced by Tyr. FY3 contains 562 amino acids with a Met at position 1 and Ala at position 2, corresponding to the Met and Ala of positions 271 and 272, respectively, of the wild type enzyme. FY4 corresponds to the T. thermophilus DNA polymerase lacking the N-terminal 274 amino acids having a Phe to Tyr replacement at position 396 (position 669 of the wild type enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase lacking 5^{\prime} to 3^{\prime} exonuclease activity
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This sequence encodes a thermostable DNA polymerase of the invention. The thermostable polymerases of the invention are variants of Tag DNA polymerase having a Tyr residue at a position corresponding to Tag DNA polymerase residue 667 in its dNMP binding site, and lacking 5' to 3'
                                                                                                                                                                                                                                                                                                                                                          14-MAY-1996;
31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5885813-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FY2 polymerase coding sequence
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                                                                                                                                            New thermostable DNA polymerases - having and lacking 5' to 3' exonuclease activity
                                                                                                                                                                                                                                                                          Cunniff JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FY2 polymerase;
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                                                                                                     Claim 7; Column 11-16;
                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                 WPI; 1999-228538/19
                                                                                                                                                                                                                                                                                                               (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuSer***GluLeu***IleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing;
                                                                                                                                                                                                             AAY00886.
                                                                                                                                                                                                                                                                          Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                          96US-0648657.
95US-0455686.
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44.00
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93.62%
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                                                                                                   27pp; English.
                                                                                                                                                                                                                                                                          Fuller CW,
                                                                                                                                                                - having 540 to 582 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taq polymerase variant;
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CC exonuclease activity as a result of an N-terminal deletion. The CC automated means.

XX

SQ sequence 1686 BP; 283 A; 567 C; 578 G; 258 T; 0 other;

Alignment Scores:
Pred. No.:

44.00
Percent Similarity:
Percent Similarity:
B1.828
Query Match:
DB:

US-09-823-649A-2 (1-11) x AAX27130 (1-1686)

QY 1 LeuSer***GluLeu****IleProTyrGluGlu 11
Db 1219 CTCTCCCAGGAGCTAGCATCCCTTACGAGGAG 1251

Search completed: January 15, 2003, 12:55:25

Search completed: January 15, 2003, 12:55:25
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RESULT 2
AAB47794
ID AAB4
XX AAC AAB4
XX DT 25-1
XX NAT
DT 25-1
XX NAT
CON Th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB47794 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 3; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using a mutant thermoactive DNA polymerase
                            Claim 4; Page 4; 23pp; English
                                                                                                                                                                                                                                                                         Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                         Smith ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001; 2001EP-0109341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1152062-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Native DNA polymerase motif #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB47794;
                                                                                                                                                                                                                                                                                                                                                                (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
                                                                                                                                                                                                                2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                         Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Gln, Gly
                                                                                                                                                                                                                                                                   m CM, Gelfand DH,
Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 23;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                         rrj
                                                                                                                                                                                                                                                                                                      Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                         Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases from Thermus species flavus, sps17 and filiformis.
                                                                                                                                                                                                     DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription.
                                                                                                                                                                                                                                                                                                                                                                    RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
Sequence
11 AA;
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AAM48259
                  RESULT 3
                                                                                  Matches
                                                                                                   Query Match
                                                                                           Local Similarity
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1 LSXELSIPYEE 11
                                                              1 LSXELXIPYEE 11
                                                                                 10;
                                                                                  Conservative
                                                                                          93.6%;
90.9%;
11 AA
                                                                                          Score 44;
Pred. No.
                                                                                 0; Mismatches
                                                                                           0.011;
                                                                                                    DB 23;
                                                                                                   Length 11;
                                                                                 Indels
                                                                                 0;
                                                                                 Gaps
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B γ

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DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
                                                                                                                                                                                                                                                                                                              Native DNA polymerase motif #8.
                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM48259 standard; Peptide;
07-NOV-2001.
                                                              EP1152062-A2
                                                                                                                   Thermus aquaticus
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Schoenbrunner NJ, Wang AM; Smith ES, Elfstrom CM, (HOFF ) HOFFMANN LA ROCHE & CO AG F. Gelfand DH, Higuchi RG, Myers

18-APR-2000; 2000US-198336P 12-APR-2001; 2001EP-0109341.

WPI; 2002-076891/11.

Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a musing a mutant thermoactive DNA polymerase a mixture

Disclosure; Page 7; 23pp; English.

The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is

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                                                                                                                                                                                                                                                                                                                                                RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods and provides without the previous full temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2002
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                                                                                                                                             transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcriptase polymerase chain reaction ampusing a mutant thermoactive DNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith ES,
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                                                                                                                                                                                                                                                                                                                concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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nes 9; Conserv
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mixture
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Sequence

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AA;

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RESULT 5
AAAM48261
AC AAAM4
XXX AAM4
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PP 1 12
PP 2 12
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                                                                                                                                                                                                                                                                                          concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA polymerase; reverse transcription; primer; divalent cation; mulant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Native DNA polymerase motif #10.
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                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motils represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAH47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. "The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reverse transcribing an RNA, comprises performing a retranscriptase polymerase chain reaction amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenbrunner NJ, Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                       1 LSXELXIPYEE
                                                                                                                                                                                                                                     11 AA;
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23pp; English.
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81.8%;
                                                                                                                                              93.6%;
81.8%;
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                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 0.011;
                                                                                                                                           Score 44; DB 23; Pred. No. 0.011;
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                                                                                                                  Mismatches
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RESULIT 7
AAM48263
ID AAM4
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AC AAM4
XX
AC AAM4
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XX
                                                                                                                                           Query Match
Best Local Similarity
----hes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                          The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse transcribing an \overline{K}NA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48262;
           25-MAR-2002
                                 AAM48263;
                                                     AAM48263 standard; Peptide; 11
                                                                                                                                                                                                                                 transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                               useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                              polymerase. These motifs represent a conserved region which affects DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus species Z05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Native DNA polymerase motif #11.
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                                                                                                                                                                                                                        needed for the reaction.
                                                                                                                                                                                                                                                                                                                                  RNA, a primer, a divalent cation, and a mutant thermoactive DNA
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                                                                                                            ш
                                                                                                                              1 LSXELXIPYEE 11
                                                                                                           LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elfstrom CM,
                                                                                                                                                                                                   11 AA;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang AM;
                                                                                                                                                                 93.6%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelfand DH,
                                                                                                                                                        0;
                                                                                                                                                       Score 44; DB 23; Length 11; Pred. No. 0.011; o; Mismatches 2; Indels
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                                                                                                                                                       Gaps
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                                                                                                                                                                 RESULT 8
AAM48264
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith ES,
   EP1152062-A2
                                           dye; amplification.
                                                                                     Native DNA polymerase motif #13.
                                                                                                          25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                             1 LSQBLISTPYEE 11
                                                                                                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                                                                                                        Conservative
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DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                          WPI; 2002-076891/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus species sps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Native DNA polymerase motif #12
                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                               Elfstrom CM,
                                                                                                                                                                               Wang AM;
                                                                                                                                                                                                               Gelfand DH,
                                                                                                                                                                                                               Higuchi RG,
                                                                                                                                                                                                               Myers TW;
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provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster treating a transverse transcription, and antiant thermoactive DNA RNA, a primer, a divalent cation, and a nutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the polymerase. These motifs represent a conserved region which affects the polymerase. The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an NNA, comprises treating a transverse transcription reaction mixture which comprises the DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method reverse transcription extension rates, and consequently less time is the reaction.

1 LSXELXIPYEE 11

93.6%;

Score 44; DB 23 Pred. No. 0.011; Mismatches

DB 23;

Length 11; Indels

0; Caps

0;

0;

AAM48264 standard; Peptide; 11 AA

DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;

Thermus caldophilus

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RESULT 9
AAM48265
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                            dye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently loss time is
           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                    18-APR-2000; 2000US-198336P
                                                                                      07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-076891/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith ES,
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                                                            12-APR-2001; 2001EP-0109341
                                                                                                             EP1152062-A2
                                                                                                                                   Thermus filiformis.
                                                                                                                                                                                    DNA polymerase; reverse transcription; primer; divalent cation; mutant,
                                                                                                                                                                                                           Native DNA polymerase motif #14.
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                                                                                                                                                                      transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          concentrations relative to previous high temperature reverse
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                                                                                                                                                                                                                                                                                                                                                                         1 LSXELXIPYEE 11
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                                                                                                                                                            amplification
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
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           N-PSDB; AAT27686
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RESULT 10
AAR96267
ID AAR96
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Best Local
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09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mulant DNA polymerase provides faster
                                 Oldenburg MC, Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith ES, Elfstrom CM, Schoenbrunner NJ, Wang
WP1; 1996-259862/26.
                                                                                                                                                                                                                           09-NOV-1995;
                                                                                                                                                                                                                                                                                                    W09615267-A1
                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus; identification; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Thermus aquaticus DNA polymerase (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR96267 standard; Protein; 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reverse transcription extension rates, and consequently less time is needed for the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 7; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reverse transcribing an RNA, comprises performing
                                                        Brow MAD,
                                                                                          (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                               23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                            Escherichia, Saccharomyces, Campylahacter,
                                                                                                                                                                                                                                                                                                                                                                                                              p53; mulant; mutation; cleavage; nuclease; cleavase; Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR96267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSQELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRAMINIANS !!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AA;
                                                     Dahlberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                             95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                         95WO-US14673.
                                   JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gelfand
                                                     Fors L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 23
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DH,
                                                      Heisler LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                     Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 11
ARR23145
ID AAR23
XX ARA23
XX DT 22-O(
DT 22-O(
DT 22-O(
DT Muta
XX Muta
XX FT Mis.
FT Mis.
FT Mis.
FT Mis.
FT Mis.
FT SX XX
XX WO:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                          28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes we a created from that construct. This mutant was created
      Abramson RD,
                                                                                                                                                                                                                                                                                                                                16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                              W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant thermostable DNA polymerase enzyme MET-SER 290 Taq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR23145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23145 standard; Protein; 544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPEC to trim both 3 overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. This mutant Taq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternatively, microbial gene sequences. Cleavage products as compared to the cleavage products of reference gene sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RIM) BN enzyme, Thermus aduatious DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae polymerase, Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2A; Page 287-288; 433pp; English
                                                             (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially hepatitis C virus and simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rad1/Rad10 complex. The nucleic acid substrate is preterably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
      Gelfand DH;
                                                                                                                          90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                                                                                                                                91WO-US07035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "deletion of residues 2-289 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This mutant was created and BamHI. The DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

Qy

Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays N-PSDB; AAQ23998.

WPI; 1992-150885/18.

esp. in human p53 gene, to identify strains of microorganisms and

Claim 11; Page 59; 185pp; English

detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare to a complete lack of activity. See also AAR23140-79 and AAR23722. a range of recombinant proteins having 5'-3' exonuclease activity discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA The sequence is that of a mutant of Thermus aquaticus polymerase mutant MET-SER 290 Taq (the Stoffel fragment) baving a different in enzymes used in homogeneous assays for the amplification and techniques, esp. nucleic acid amplification by PCR, self-sustained

Sequence 544 AA;

В Qγ Matches Best Local Similarity Query Match 390 LSQELAIPYEE 400 1 LSXELXIPYEE 11 Conservative 93.6%; 0; Mismatches Score 44; DB 13; Length 544; Pred. No. 0.89; Gaps 0,

RESULT 12 AAR23163 22-OCT-1992 (first entry) AAR23163; AAR23163 standard; Protein; 544 AA

Mutant thermostable DNA polymerase enzyme MET-ALA 292 TZ05.

5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR

Thermus species 205

16-APR-1992. WO9206200-A.

30-SEP-1991; 91WO-US07035

28-SEP-1990; 28-SEP-1990; 90US-0590213. 90US-0590466. 90US-0590490.

(CETU ) CETUS CORP. 28-SEP-1990;

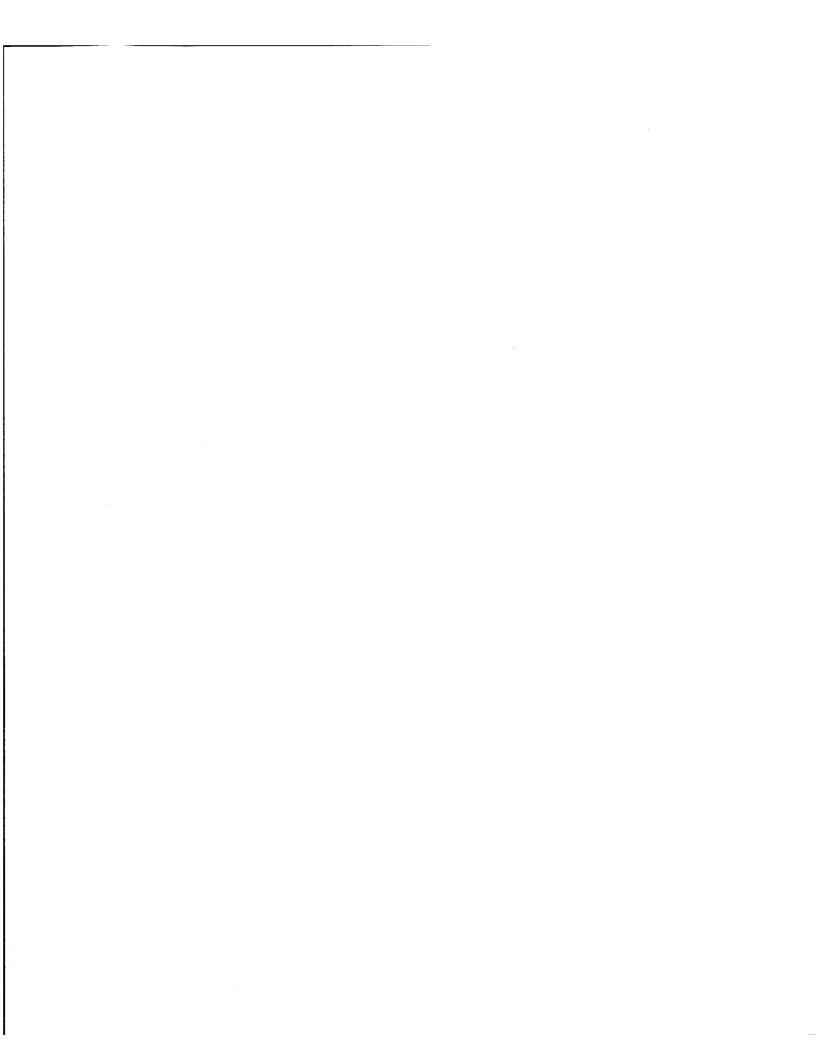
Abramson RD, Gelfand DH;

N-PSDB; AAQ24322. WPI; 1992-150885/18.

in e.g. PCR, sequencing and detection assays activity - having conserved regions mutated or deleted, for use Thermostable DNA polymerases with altered 5'-3' exo nuclease

Claim 11; Page 59; 185pp; English

ΡŢ Cleavage of nucleic acids to detect mutation/s) - allows detection



X00000000000000000XX

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RESULT 13
AAR23168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a mutant of Thermus species Z05 polymerase mutant MET ALA 292 TZ05, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinations having 5'-3' exonuclease activity to a complete lack of
The sequence is that of a mutant of Thermus thermophilus polymerase mutant MET-ALA 292 Tth. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                           Claim 11; Page 59; 185pp; English.
                                                                                                            activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                        N-PSDB; AAQ24328.
                                                                                                                                                                                                             WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'-3'; exonuclease; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant thermostable DNA polymerase enzyme MET-ALA 292 Tth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR23168 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                  Thermostable DNA polymerases with altered 5'-3' exo nuclease
                                                                                                                                                                                                                                                   Abramson
                                                                                                                                                                                                                                                                                                                                            28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also A \land R23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                     (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                            28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 LSCELAIPYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermophilus
                                                                                                                                                                                                                                                   RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                       CORP.
                                                                                                                                                                                                                                                 Gelfand
                                                                                                                                                                                                                                                                                                                          90US-0590490
                                                                                                                                                                                                                                                                                                                                              90US-0590213.
90US-0590466.
                                                                                                                                                                                                                                                                                                                                                                                                    91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "residues 2-291 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.6%;
                                                                                                                                                                                                                                                   멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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AAR23157
   CCCCCXXXXXIII
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Best Local
amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined
                                                                     The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 288 Tsps17, having a different amt. of 5'-3' exonucles activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                       are useful
                                                                                                                                                  Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                          Thermostable DNA polymerases with altered 5'-3' activity - having conserved regions mutated or d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR23157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity.
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many recombinant DNA techniques, esp. nucleic

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exonuclease

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are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chair reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus species
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant thermostable DNA polymerase enzyme MET-ALA 288 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1992
                                                                                                                                   28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                             30-SEP-1991;
                                                                                                                                                                                                                                                                                        W09206200-A
                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAR23140-79 and AAR23722
N-PSDB; AAQ24010
                  WPI; 1992-150885/18
                                                                                                                                                                                                                                                    16-APR-1992
                                                      Abramson RD,
                                                                                            (CETU ) CETUS
                                                                                                                                                                         28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 LSQELAIPYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                            CORP.
                                                      Gelfand
                                                                                                                                                       90US-0590466
                                                                                                                                                                         90US-0590213.
                                                                                                                                     90US-0590490
                                                                                                                                                                                                             91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                           SPS17
                                                                                                                                                                                                                                                                                                                                               /note= "residues 2-287 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.6%;
                                                      DH;
                                                                                                                                                                                                                                                                                                                            sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Best Local
                                         The invention relates to a chimeric nucleic acid polymerase comprising at least two enzymatically active domains which are non-naturally associated. The polymerase is thermostable and possesses new or improved catalytic properties compared to known nucleic acid polymerases. The polymerase eliminates the need to specifically develop multi-enzyme reaction mixtures, which are often difficult to optimise and expensive to use. The polymerase facilitates rapid, efficient and accurate generation of nucleic acid molecules, particularly in regard to PCR protocols. The polymerase is also useful for nucleic acid polymerisation which is useful in genetic engineering techniques and molecular biology.
                                                                                                                                                                                                                                                                      Chimeric nucleic acid polymerase for nucleic acid polymerization and generation of nucleic acids, comprises two enzymatically active domains which are non-naturally associated \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase ligase chain reaction (PICR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                         Claim 12; Page 46-49; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus aquaticus; Taq; DNA polymerase; polymerisation; PCR protocol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                              The present protein sequence is Thermus aquaticus (Taq) DNA polymerase
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-536571/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000; 2000US-0506153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2001; 2001WO-EP01790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus aquaticus (Taq) DNA polymerase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09304 standard; Protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                              Loeffert D,
                                                                                                                                                                                                                                                                                                                                                                                                               (QIAG-) QIAGEN GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200161015-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 LSQELSIPYEE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 81.0 hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545 AA;
                                                                                                                                                                                                                                                                                                                                                                              Missel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                              Kang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1
Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,:
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Query Match Best Local

Sequence

552 AA;

Matches

Similarity9; Conserve

Conservative

93.6%;

Score 44; DB 22; pred. No. 0.9; 0; Mismatches 2

2:

Indels

0,

Gaps

0,

Length 552;

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Дb
                20
398 LSQELAIPYEE 408
                  LSXELXIPYEE 11
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Search completed: January 15, Job time: 30.2857 secs 2003, 11:20:14

Sequence Sequence

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sequence sequence

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Appli Appli

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-823-649A-2
47
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       January 15, 2003, 11:17:28; Search time 9.28571 Seconds (without alignments) 34.855 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSXELXIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length DB
      US-08-484-956-90
US-08-520-96-399-2
US-08-520-6-399-2
US-08-08-021-6-32C-6
US-09-096-399-2
US-08-021-6-32C-6
US-09-096-399-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-4
PCT-US95-14418-6
US-09-777-537-2
US-09-777-538-2
US-09-777-538-6
US-08-4819-6
US-08-4819-6
US-08-4819-6
US-08-481-388-5
US-08-481-388-5
US-08-481-388-5
US-08-481-55-386-5
US-08-823-516-5
US-08-823-516-5
US-08-823-516-5
US-08-823-516-5
US-08-823-516-5
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Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
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US-08-484-956-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
                                                                                            FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARRPOLL ], PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                    TELEPHONE: (415) 705-8410
                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLDENBURG, MARY C. APPLICANT: HEISLER, LAURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 E.C. CLITY: SAN FRANCISCO
                                                        REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
    TELEFAX: (415) 397-8338
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: HAVERSTOCK, MEDLEN & CARROLL 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES
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US-08-758-314-5
US-09-350-309-5
US-08-520-946-5
US-08-156-020-2
US-08-156-020-6
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Sequence Sequence Sequence

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; Sequence 90, Application US/08520946
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Best Local Similarity
                                                                                                                                                Matches
                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kyamichev, Wichael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTALTION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                              374 LSQELAIPYEE 384
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STATE:
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Local Similarity 81.8%;
les 9; Conservation
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                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/757,653 FILING DATE:
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                                                                                                             1 LSXELXIPYEE 11
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California
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81.8%;
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                                                                                                                                                             Score 44; DB 2; Length 528; Pred. No. 0.34;
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Pred. No. 0.34;
                                                                                                                                                Mismatches
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; OTHER INFORMATION: Recombinantly engineered mutant \ensuremath{\text{US-09-096-399-2}}
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APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
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US-09-096-399-2
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; Patent No. 6130045
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Query Match
Best Local Similarity bi...
Conservative
                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 553
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/096,399A CURRENT FILING DATE: 1998-06-11
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                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Thermostable Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHBY, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTIVE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/520,946
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(415) 397-8338
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                     93.6%; Score 44; DB 4; Length 553;
81.8%; Pred. No. 0.36;
ative 0; Mismatches 2; Indels
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Pred. No. 0.34;
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                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
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                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                      Sequence 4, Application US/09096399A Patent No. 6130045
                                                                                                                       APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
TITLE OF INVENTION: Thermostable Polymerase
                                                                         CURRENT APPLICATION NUMBER: US/09/096,399A CURRENT FILING DATE: 1998-06-11
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                                                           NUMBER OF SEQ ID NOS: 4
                                                                                                          FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
TYPE: PRT
                ENGTH: 559
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk, 5.25",
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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One Metropolitan Square, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 amino acids
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WENTION: Thermostable DNA polymerase with

WENTION: enhanced thermostability and enhanced length and

WENTION: efficiency of primer extension
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81.8%;
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Pred. No. 0.36;
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PCT-US95-15327-5
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: OTHER INFORMATION: Recombinantly engineered mutant US-09-096-399-4
                                                                                                                                   Sequence 5, Application PC/TUS9515327 GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity 81.8%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                   APPLICANT:
TITLE OF INVENTION: Bio
TITLE OF INVENTION: The
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/14418
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312/474-0448
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81.8%;
                                                     Biologically Active Fragments
Thermus Flavus DNA Polymerase
51
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Pred. No. 0.
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Pred. No. 0.37;
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South Wacker Drive
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Query Match
Best Local Similarity
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GENERAL INFORMATION:
            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENCTH: 597 amino acids
TYPE: amino acid
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LENGTH: 560 amino acid
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NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
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RAME: Gass, David A.
REGISTRATION UNDBER: 38,153
REFERENCE TOCKET NUMBER: 28003/31716
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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TYPE: ami
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CLASSIFICATI
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STATE: Illinois
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CLASSIFICATION:
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/14418
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linear
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81.8%;
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Pred. No. 0.37;
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US-09-587-856-2
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SOFTWARE: SEQ ID NO 2
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                               Sequence 2, Application US/09587856 Patent No. 6214557
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Best Local Similarity

Matches 9; Conserv
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Matches 9; Conserv
                       CURRENT APPLICATION NUMBER: US/09/587,856
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
                                                                                             APPLICANT: Washington University TITLE OF INVENTION: COLD SENSITIFILE REFERENCE: WSHU 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               Type: amino acids
Type: amino acid
TopoLogy: line
WOLECUTE
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LENGTH: 597 amino acid
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                           COLD SENSITIVE MUTANT DNA POLYMERASES
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81.8%;
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81.8%;
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    Mismatches

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Pred. No. 0.39;
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678 LSQELAIPYEE 688

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                                                                                                               ; TYPE: PRT ; ORGANISM: Thermus aquaticus US-09-777-538-2
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SEQ ID NO 2
LENGTH: 810
TYPE: PRT
ORGANISM: Thermus aquaticus
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                                                                               Query Match
                                                                                                                                                                            SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/777,538
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 09/587,856
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                   APPLICANT: Barnes, Wayne M
APPLICANT: KermeKchiev, Milko B
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: WSHU 2009.2
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PRIOR APPLICATION NUMBER: 09/587,856
PRIOR FILING DATE: 2000-06-06
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CURRENT FILING DATE: 2001-02-06
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TITLE OF INVENTION: NUCLEIC ACIDS ENCODING COLD SENSITIVE MUTANT DNA
TITLE OF INVENTION: POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
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Local Similarity 81.8%;
hes 9; Conservative
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                  1 LSXELXIPYEE 11
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                                                                93.6%;
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81.8%; Pred. No. 0.55;
tive 0; Mismatches
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                                                Score 44; DB 4;
Pred. No. 0.55;
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Pred. No. 0.55;
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RESULT 14
US-07-977-434-6
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TITLE OF INVENTION:
                                                                   ATTORNEY/AGENT INFORMATION: NAME: Luann Cserr
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
                                REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: Case No.
                                                                                                                                                   APPLICATION NUMBER: US 61 FILING DATE: 02-NOV-1990
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5' TO 3' EXONUCLEASE MUTATIONS OF THERMOSTABLE DNA POLYMERASES
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                                                                                                                   US 557,517
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Query Match
Best Local Similarity
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US-08-458-819-6
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APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
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                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 15-AUG-1
                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-JUN-1987
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US,
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APPLICATION NUMBER: US 55
FILING DATE: 28-SEP-1990
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APPLICATION NUMBER:
                               APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
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07110-1199
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UMBER: US 590,490
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Search completed: January 15, 2003, 12:38:22 Job time :  $11.2857 \ \text{secs}$ 

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Query Match
Best Local Similarity
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                                                                                                             ; MOLECULE TYPE: protein US-08-458-819-6
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acid
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 557,517
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
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676 LSQELSIPYEE 686
                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,822
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                                                                 Score 44; DB 1;
Pred. No. 0.56;
                                                       Mismatches
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Sequence 6, Sequence 6, Sequence 6,

Appli Appli

Sequence 6, Appli Sequence 11, Appl Sequence 15, Appl Sequence 23, Appli Sequence 24, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 37, Appli Sequence 37, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 38, Appli

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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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US-10-081-806-4
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                                             RESULT 2
US-09-823-649A-4
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                                                                                                                                                                                                                                                   ; OTHER INFORMATION: sequence motif US-09-823-649A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, Edward
APPLICANT: Elfstrom, Carita
APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russell
APPLICANT: Myers, Thomas
Sequence 4, Application US/09823649A Patent No. US20020012970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentlu version 3.0 SEQ ID NO 3
                                                                                                                                                                                   Matches
                                                                                                                                                                                                  Query Match
Best Local
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APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: RPA1006
CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,346
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US-09-735-169A-2

US-09-735-171A-2

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US-09-925-302-585

US-10-062-254-37

US-09-854-845-19
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Sequence 9, Application US/09823649A
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                       SEQ ID NO 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
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                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Thermus aquaticus
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Elfstrom, Carita
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Schoenbrunner, Nancy
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APPLICANT: Elfstrom, Cari
APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russe
APPLICANT: Myers, Thomas
APPLICANT: Schoenbrunner,
GENERAL INFORMATION:
APPLICANT: Smith, Edward
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Best Local Similarity
Matches 9; Conserv
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PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                                           LENGTH: 11
TYPE: PRT
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Gelfand, David
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Pred. No. 0.0021;
0; Mismatches
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Pred. No. 0.0021;
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US-09-823-649A-13; Sequence 13, Application US/09823649A; Patent No. US20020012970A1
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: Sequence 12, Application US/09823649A

: Patent No. US20020012970A1 *
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                                                                    GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
 APPLICANT:
                                                    APPLICANT: Smith, Edward
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APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russell
APPLICANT: Myers, Thomas
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TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Thermus sp. sps17
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Elfstrom, Carita
Gelfand, David
Higuchi, Russell
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Gelfand, David
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Pred. No. 0.0021;
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US-10-033-297-5
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; LENGTH: 11
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                                                                                                                               Sequence 5, Application US/10033297 Publication No. US20020187486Al
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
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APPLICANT:
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TITLE OF INVENTION: HICH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMPTILE REFERENCE: REALOO6
FILE REFERENCE: REALOO6
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                                                                  AL INFORMATION:
APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
            Brow, Mary Ann D.

TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 163
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Schoenbrunner, Nancy
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Gelfand, David
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                                                              Mast, Andrea L.
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81.8%;
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Pred. No. 0.0021;
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Pred. No. 0.0021;
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US-10-081-806-5; Sequence 5, Application US/10081806; Publication No. US20020197623A1
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                        CORRESPONDENCE ADDRESS:
                                                                                                  Hall, Jeff G.
Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
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                                                                                                                                                                  APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/350,597
FILING DATE: 09-Jul-1999
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                         ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/599,491 FILING DATE: 24*JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/756,386 FILING DATE: 29-NOV-1996
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APPLICATION NUMBER: US 08/758,314
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FILING DATE: 12-No. US20020187486A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
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Pred. No. 0.22;
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COUNTRY: United States Of America
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Sequence 4, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
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           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hall, Jeff G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 8
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                  COUNTRY: United States Of America
                                                                                                                                                                                                                                            STATE: California
                                                                                                                                                                                                                                                                                 STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                                                                                                                                                                                                                                                            San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yamichev, Victor 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397-8338
                                                                                                                                                                                                                                                                                                                                                                           Sequential Invasive Cleavages
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Pred. No. 0.22;
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Sequence 2, Application US/09972834
Publication No. US20020192663A1
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                                                       MEDIUM TYPE: Floppy disk
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/09/972,834
FILING DATE: 04-Oct-2001
CLASSIFICATION: GUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: NO. US20020187486A1 Relevant
TOPOLOGY: NO. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
3-297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Loeb, Lawrence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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FILING DATE: 12-UUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
  APPLICATION NUMBER: 08/978,806 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                  COUNTRY: United States
                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                                                           CITY: San Diego
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/756,386 FILING DATE: 29-NOV-1996
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APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 832 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/10071505; Publication No. US20020197211A1; GENERAL INFORMATION:
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                                                                                                                                                                                                      US-10-081-806-4
                                                                                                                                                                                                                           RESULT 15
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                                                                                                                                         Sequence 4, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local Similarity 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Flick, Parke
TITLE OF INVENTION: TAO DNA Polymerase Having an Amino Acid Substitution at
TITLE OF INVENTION: E681 and Homologs Thereof Exhibiting Improved Salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EDITITLE OF INVENTION: TO FILE REFERENCE: PB9944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/071,505
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathry
                     CORRESPONDENCE ADDRESS:
                                    Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBER OF SEQUENCES: 69
                                                                                                   APPLICANT: Prudent, James R. Hall, Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A.
REFERENCE/DOCKET NUMBER: P-UW 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619)535-8949
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Nampalli, Satyam
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Pred. No. 0.22;
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Pred. No. 0.22;
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678 LSQELAIPYEE 688

US-10-033-297-4

Matches Query Match

Local Similarity nes 9; Conserv 1 LSXELXIPYEE 11

US-09-972-834-2

GENERAL INFORMATION:

RESULT 13

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Search completed: January 15, 2003, 12:39:50 Job time: 10.8571 secs
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                                                           Qy
                                                                                 Query Match
Best Local S
Matches 9
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CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURKENT APPLICATION NUMBER: US/10/081,806
FILING DATE: 22-Feb-2002
CLASSIFICATION: CUNKNOWN>
                                        678 LSQELAIPYEE 688
                                                                                  Local Similarity
nes 9; Conserv
                                                     1 LSXELXIPYEE 11
                                                                                 Conservative
                                                                                           93.6%; Score 44; DB 9; Length 832; 81.8%; Pred. No. 0.22;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    protein search, using sw model

     length: 2000000000
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S75715
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T40331
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1 LSXELXIPYEE 11
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## ALIGNMENTS

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A;Molecule type: DNA
A;Residues: 1-831 <ISH>
C;Superfamily: DNA-directed DNA polymerase
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                  C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999 C:Accession: JX0359
C:Accession: JX0359
R:IShino, Y:, Ueno, T:, Miyagi, M.; Uemori, T.; Imamura, M.; Tsunasawa, S.; Kato, I.
J. Biochem. 116, 1019-1024, 1994
A:Tittle: Overproduction of Thermus aquaticus DNA polymerase and its structural analys
A:Reference number: JX0359; MUID:95204371; PMID:7896728
A:Accession: JX0359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: polI
C;Superfamily: DNA-directed DNA polymerase I
C;Keywords: DNA binding; nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X66105; A; Note: the source is designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-831 <AKH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20, 5839, 1992

A;Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from A;Reference number: S26675; MUID:93087201; PMID:1454544
                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S26675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus
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    Similarity 9; Conserv.
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81.8%;
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Pred. No. 0.46;
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Pred. No. 0.46;
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: G70332
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                    A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666; PMID:9537320 A; Accession: G70332
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A;Title: Isolation, characterization, and expression in Escherichia coli of the A;Reference number: A33530; MUID:89197950; PMID:2649500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Thermus aquaticus
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 18-Jun-1999
   A;Status:
                                                                           Nature 392,
                                                                                                           R; Deckert, G.; Warren, P.V.;
                                                                                                                                                                                conserved hypothetical protein aq_367 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SGD: PCL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-229 <LAT>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Latreille,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-832 <LAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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   preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                         LNYELAIPYDE 184
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81.8%;
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                                                                                                           T.; Young,
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A;Molecule type: DNA
A;Residues: 1-474 <KUR>
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D98157
                                                  A; Map position:
C; Superfamily: n
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A; Accession: D98157
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C; Superfamily: n
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R;Wood, D.W.; Setuba
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Query Match
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"hes 6; Conservative
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                                                              A;Cross-references: GB:AE007870; PIDN:AAK88782.1; PID:g15158531; GSPDB:GN00170 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                              A; Title: Genome Sequence
                                                                                                                                                                                                                                  Science 294, 2323-2328,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain
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A; Residues: 1-457 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193
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C; Species: Agrobacterium tumefaciens
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A; Residues: 1-850 <AQF>
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                                                                                                                                                                                                                                , B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurol
F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas,
94, 2323-2328, 2001
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                                                                                                                                                                                        uence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A97359; PMID:11743194
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Markelz,
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78.7%; 63.6%;

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DB 2; 7.1;

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"Cloning of rat alpha-2-B-ddrenergic receptor gene and expression in rat submandibular gland.";
Shigaku 80:317-326(1992).
-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation.
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PIR; S13023; S13023.
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EMBL; X57659; CAA40861.1; -.
EMBL; M62371; AAA42033.1; -.
EMBL; D00819; BAA00700.1; -.
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SIMILARITY: BELONGS TO
                                               LXXXXXXXXXX 11
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
           LAAALAAAAAE 16
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                                                                                                    Similarity
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                                                                                                                                                          458 AA;
                                                                                  Conservative
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18.2%;
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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RPN4_YEAST
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InterPro; IPRO00822; Znf_C2H2.

Pfam; PF00096; Zf-C2H2; 2.

SMARR; SM00355; Znf_C2H2; 1.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.

Proteasome; Nuclear protein.

Proteasome; Nuclear protein.

DOMAIN 300 315

ASP/GLU-RIC
DOMAIN 382 398

NUCLEAR LOC
                                                                                                                                                                                         EMBL; Z48432; CAA8833
EMBL; Z74068; CAA9857
PIR; S30806; S30806.
PIR; S41986; S41986.
                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PMOT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson M.K., Kurihara T., Silver P.A.; "Extragenic suppressors of mutations in the cytoplasmic C SEC63 define five genes in Saccharomyces cerevisiae."; Genetics 134:159-173(1993).
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                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae."; FEBS Lett. 423:149-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95340540; PubMed=7615550; Johnson E.S., Ma P.C.M., Ota I.M., Varshavsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93292918;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993
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                                                                                                                                                                                                                                                                                                                            entitles requires a
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"Sonip is a component of the 26S proteasome of the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98171302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
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16-OCT-2001 (Rel. 40, Last annotation update)
26S proteasome regulatory subunit RPN4 (Nuclear protein SON1)
                                                                                                                                                        SGD; S0002178; RPN4.
                                                                                                                                                                             TRANSFAC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 270:17442-17456(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MAY PLAY A ROLE IN NUCLEAR INTEGRITY, IS REQUIRED FOR NORMAL GROWTH AT LOW TEMPERATURES. SON1 MUTANTS GROW SLOWLY AT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LUCATION: Nuclear.
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an email to license@isb-sib.ch).
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CAA98579.1;
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01-APR-1988 (Rel. (
01-FEB-1991 (Rel. 1
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                                                                                                      Viruses; dsDNA viruses, no phi-29-like viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the late region of Bacillus phage phi completes the 19,285-bp sequence of phi 29 genome. Comparison the homologous sequence of phage PZA.";
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phi-29-like viruses.
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01-FEB-1991
SEQUENCE FROM N.A.
MEDLINE-87031573; PubMed-3095188;
Paces V., Vlcek C., Urbanek P.;
"Nucleotide sequence of the late region of Bacillus subtilis phage
                                                                                                                                             Bacteriophage PZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                            Pre-neck appendage protein (Late protein GP12).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373D4F4275D73EED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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YM8G_YEAST
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID~4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YM8G_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M11813;
                                                                     PRANSMEM
                                                                                                                        TRANSMEM
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2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854 AA;
                                                                                                                                                                                                           1 protein;
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SE DRE COCCOCCO
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Gene 44:107-114(1986).
                                                                                                                                                                                                                                                                                 InterPro; IPR003864; DUF221. Pfam; PF02714; DUF221; 1.
                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE YLL005C/YMR266W/Y0L084W FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lye G., Churcher C.M., Barrerr B.G., May-1995) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01.NOV-1997 (Rel. 35, Last sequence update)
01.NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 107.7 kDa protein in TSP3-IPP2 intergenic region.
YMR266W OR YM8156.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long as its content
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    107672 MW;
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F6F7BA2B3F3AD44B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953 AA
                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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Query Match
Best Local Similarity
Watches 2; Conserva
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E4L2_MOUSE
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Search completed: January 15, 2003, 11:21:14 Job time: 13.2857 secs
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Best Local Similarity 18.2%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.

SMART; SM00295; B41; 1.

PROSITE; PS00660; BAND.41_2; 1.

PROSITE; PS00661; BAND_41_2; 1.

PROSITE; PS0067; BAND_41_3; 1.

Structural protein; Cytoskeleton.

STRUCTURAL PROSITE; PS0067; BAND 41_3; 1.

STRUCTURAL PROTEIN; CYTOSKELETON.

DOMAIN 208 422

DOMAIN 489 651

DOMAIN 652 837

SPECTIP

DOMAIN 652 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E41.2_MOUSE STANDARD; PRT; 988 AA.

070318;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Band 4.1-11ke protein 2 (Generally expressed protein 4.1) (4.1G).
Band 4.1-11ke protein 2 (Generally expressed protein 4.1) (4.1G).
Band 4.1-11ke protein 2 (Generally expressed protein 4.1) (4.1G).
BEPB41L2 OR EPB4.1L2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walensky L.D., Gascard P., Fields M.E., Blackshaw S., Conboy J.G., Mohandas N., Snyder S.H.;
"The 13-kD FX506 binding protein, FKBP13, interacts with a novel homologue of the crythrocyte membrane cytoskeletal protein 4.1.";
J. Cell Biol. 141:143-153(1998).
-:- SUBUNIT: The CTD domain interacts with FKBP-13.
-:- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF044312; AAC40083.1; -. MGD; MGI:103009; Epb4.112. InterPro; IPR000299; Band_4.1. Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Sunstantian institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=98198473; PubMed=9531554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                      720 LSSESSSSSSE 730
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                                                                                                                                                                                                                                                                                                                   988 AA;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                   109833 MW; B0367A16C5A2EC05 CRC64;
                                                                                                                                                                                                                                     44.4%; Score 8; DB 1; Length 988; 18.2%; Pred. No. 1.4e-06;
                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                 HYDROPHILIC.
SPECTRIN--ACTIN-BINDING.
CARBOXYL-TERMINAL (CTD).
                                                                                                                                                                                                                                                                                                                                                                                                                    BAND 4.1-LIKE.
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                          9; Indels
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Result
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Listing first 45 summaries
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Maximum DB seq length: 2
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Perfect score:
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              protein search, using sw model
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Match
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_phage:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_mammal:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_human:*
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sp_virus:*
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              101
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Q9VNY3
0 O81807
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0 Q9FH69
0 Q9H0C7
Q9H0C7
                                       Q9U0V2
Q9VC00
Q9UMS8
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060288
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                                                                                                                                                                                                                                                                                              SUMMARIES
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                                                                                                                                                                Q9j1a0 pseudorabie
Q9vny3 drosophila
O81807 arabidopsis
Q9zus8 arabidopsis
Q9fh69 arabidopsis
           Q9vc00 drosophila
Q9ums8 homo sapien
Q91143 trebouxia j
Q9nmb8 leishmania
Q8wzw6 neurospora
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Q96t25
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060288
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                                                                                                                                                                                                                                                   Description
                                                                   homo sapien
leishmania
drosophila
                                                                                                            leishmania
drosophila
                                                                                                                                       homo sapien
                                                                                                                                                    homo sapien
                                                        RESULT 2
Q9VNY3
ID Q9VP
AC Q9V
DT 01
DT 01
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Q9JIA0

ID Q9JIA1

AC QPICAT

AC Q
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Best Local Similarity 18.2
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9VNY3 PRELIMINARY; PRT; Z/4 AA.
Q9VNY3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                  STRAIN=PSEUDOKABIES VIRUS STRAIN EA;
Fang L.R., Xiao S.B., Xu J.X., Hong W.Z., Chen H.C.;
"Cloning and expression of IE180 gene of pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9J1A0 PRELIMINARY; PRT;
Q9J1A0;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last seg
01-CCT-2000 (TrEMBLrel. 15, Last ann
                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF218442; AAF43385.1; -. 101 101 101 SEQUENCE 101 AA; 10187 MW; 6E45D3887C53CA94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=10345;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudorabies virus.
                                                                                                                                                                                                                                                                                            strain."
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                                                                                                                                                                                                                                                                                                                                                                                                                                              IE180 (Fragment).
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18.2%;
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Q8UES5
Q9UHA6
Q8TD05
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Q9G0C8
Q942X0
Q9VPS9
Q9VPS8
Q9VPS8
Q87741
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Q94IH2
Q9R1L2
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Q9RWJ6
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Last annotation update)
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Q9NZH6
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Q8TD04
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                                                                                                                                                                            Score 9; DB 12; Le
Pred. No. 5.7e-14;
0; Mismatches 9;
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Q9A9K6
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                                                                                                                                                                                                      Length 101;
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O9a9k6 caulobacter
O8sbb5 oryza sativ
O9h1c6 homo sapien
O9nzh6 homo sapien
O9hbf3 homo sapien
O9hbf3 homo sapien
O9vnm9 drosophila
O9vnm9 drosophila
O94ibz nannochlori
O94ibz nannochlori
O94ibz nannochlori
O94ibz nannochlori
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Q9vps8 drosophila
Q87741 chimpanzee
Q64145 rattus sp.
Q8td04 homo sapien
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Q9vtl6 drosophila
Q9amw4 bradyrhizob
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Q8td05 homo sapien
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Q9w3s3 drosophila
Q8ues5 agrobacteri
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Q9rwj6 deinococcus
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Q9g0c8 lactococcus
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RESULT 3
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ID 0818
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DT 01-N
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Best Local
                01-NOV-1998 (TrEMBLrel. 08, Cr
01-NOV-1998 (TrEMBLrel. 08, La
01-OCT-2000 (TrEMBLrel. 15, La
Hypothetical 32.8 kDa protein.
F8D20,270 OR AT4G35760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeng J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong Y.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O., Gibhs R.A., Weers E. W. Rubin G.M., Venter T.C.
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

EMBL; AE003595; AAF51780.1; -.
EMBL; AE003595; AAF51780.1; -.
FlyBase; FB900037131; CG14564.
SEQUENCE 274 AA; 29378 MW; 9F8D2CA04755EDEB CRO
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
  Arabidopsis
                                                                                                                                                              081807;
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Eukaryota; Metazoa; Arthropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
2; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
  thaliana
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                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
18.2%;
(Mouse-ear cress).
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Last annotation updat
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Pred. No.
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9.7e-14
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Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                        Lin X., Kaul S., Konnsley S.D., Shew T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Harnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis that the communication of the plant arab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2008/487; PubMed-10617197;
Lin X., Kaul S., kounsley S.D., Shea
Fujii C.Y., Mason ".M., bowman C.L.,
Buell C.R., Ketchum K.A., Lee J.J., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Rose M., Hempel S.,
Submitted (MAR-2000)
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                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC005896; AAC98057.1; -.
                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                         "Sequence and analysis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           At2g37380 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,8SUZ96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8SDZ60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koetter P., Hempel S.,
Heijnen L., Vos P., Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koetter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                        Lin X.;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
         Local Similarity
les 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LSSSSSSTSE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis sequencing projubmitted (MAR-2000) to the EM
BL; AL031135; CAA20046.1; -.
BL; AL161588; CAB81485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
2; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (301.-1998)
                                                                                                                             321 AA;
                                                                                                                                                                                                                                                 COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                          34973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Entian
                                  50.0%;
18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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wes H.W., Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.-D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequ
         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9;
Pred. No.
                                     Pred. No.
                                                              Score 9;
                                                                                                                          7E76DD64A49CBAEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF301B0FE04AF13C CRC64;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
1e-13;
                                                              DB 10;
                                     .le-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Jesse
Schueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemcke K.,
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                              Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303,
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayer
      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosidae;
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X
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RESULT 6
Q9HCT 1
ID Q9HCT 1
AC 09HO
DT 01-M
DT 101-M
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
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                          Query Match
Best Local :
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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01-MAR-2001 (TIEMBLIFE1. 16, Last sequence update)
01-DEC-2001 (TIEMBLIFE1. 19, Last annotation update)
01-DEC-2001 (TIEMBLIFE1. 19, Last annotation update)
Genomic DNA, chromosome 5, TAC clone:K16E1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                         Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glass! Sansorge W., Becher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Kohrer K., Strack N., Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Wambutt R., Korn B., Klein M., Poustka A.; "Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                 SEQUENCE
                                                                                                                                      EMBL; AL136851; CAB66785.1; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteis
Mammalia; Eutheria; Primates; Catarrnini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 51.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H0C7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
MEDLINE-20181125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FH69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FH69
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9H0C7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004345; TB2_DP1_HVA22. pfam; PF03134; TB2_DP1_HVA22; 1. SEQUENCE 326 AA; 37321 MW; 85A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKFZP434B0535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. X. Seque features of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 LSSSSSSSSE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASSSSTAATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB022210;
. Similarity
2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7:31-63(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20181125; PubMed=10718197;
Nakamura Y., Kaneko T., K
                                                                                                                 466
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                              ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAB09327.1;
                                                                                                              51621 MW;
                          50.0%;
18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
18:2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; DB 1
Pred. No. 1.1e
0; Mismatches
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
Pred. No. 1.300; Mismatches
                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                 8B54AD1F940CBE24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85A3C1240B73506B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katoh T., Asamizu E., Kotani H.,
                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
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                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                1.3e-13
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                                                     Length 466;
  9.
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Glassi S.,
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  0;
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Matches
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Best Local
Best Local Similarity
                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BHY3;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gou D.M., Li W.X., Gao L., Sun Y.;
"A novel human zinc finger gene, hkic5.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ
EMBL; AF378304, AAK55418.1; -.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96T25;
                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TERMBLEEL. 17, Created)
01-JUN-2001 (TERMBLEEL. 17, Last sequence update)
Hypothetical 80.2 kDa protein.
15213 no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Zinc family member 5 protein.
                                                    SEQUENCE
                                                                   EMBL; AL5839:
Hypothetical
                                                                               "A physical map of the Leishmania major Friedlin Genome Res. 8:135-145(1998).
EMBL: AL583932; CAC32257.1; -.
                                                                                                                                                      MEDLINE=98146435; PubMed
Ivens A.C., Lewis S.M.,
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Huglenozoa;
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        098HY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                         Smith D.F.;
                                                                                                                                                                                                                                         Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Be Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00028; ZINC_FINGER_C2H2_1; PROSITE; PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01582; KV33CHANNEL. ProDom; PD000003; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                          STRAIN-FRIEDLIN;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
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2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 AA;
                                                  761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger
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                                                                                                                                                                        PubMed=9477341;
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                                                  80172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
18.2%;
50.0%;
18.2%;
                                                                                                                                                                                                                                                                                                                                                Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                      Bagherzadeh
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rane, hzic5.";
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Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9; Pred. No.
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                                                  3D21A6BA5E01109D CRC64;
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DB 5; I
. 1.7e-13;
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            Length 761;
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                                                                                                                   genome.";
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RESULT 9

PARSULT 9

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.I.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G.,
RA Wan K.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Belshakov S.,
Ra Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng L. B., Conter C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dordon K., Deng C., Ferraz 
              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keichum K.A., Kalmmel B.E., Kodira C.D., Kraft C., Kravilz S., Kulp D., Lai Z., Lasko P., Lei Y., Levils K.A., A., Li Z., Liang Y., Lin X., Liu X., Wattei B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Wattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.N., Pacleb J.M., Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Melson D.R., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., Reinet K., Remington K., Sunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden K., Simpson M., Skupski M.P., Smith T., Shue B.C., Stopathing A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier B., Sprakkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wassen D. R., Mang R., Mang Y., Wang A.H., Wang Y., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischma Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., 1begwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TREMBLIEL 13, 01-MAY-2000 (TREMBLIEL 13, 01-JUN-2001 (TREMBLIEL 17,
                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0030299; CG11727.
                                                                                                                                                                                                                                                                                                                                         EMBL; AE003486; AAF48044.1;
                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG11727 protein.
CG11727.
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                                                                                                                                                                                           PF00566; TBC; 1
                                                                                                                                                                 SM00164; TBC; 1.
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                                                                                                                           PS00402;
                                                                                                                                                                                                                             IPR000515; BPD_transp. IPR000195; RabGAP_TBC.
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P.G., Scherer S.E., Li P.W., Hoskins R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                      BPD_TRANSP_INN_MEMBR: UNKNOWN_1.; 92352 MW; 204F968E447D021E CRC64;
                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                  Score 9;
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01-DEC-2001
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01-AUG-1998 (Trembirel.
01-MAY-2000 (Trembirel.
01-DEC-2001 (Trembirel.
                                            STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzad
Smith D.F.;
                                                                                                                                                                                                                                                       Masuy D., Purnelle B., Goffeau A., Ivens A.C., Lawson D., Rajandream M.A., Barrell B.G.;
Submitted (DMC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            STRAIN-FRIEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible MUS308 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9U0V2;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prediction of the coding sequences of unidentified human genes. I The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Motazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIAA0540
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"A physical map of the Leishmania major Friedlin genome.";
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98290545; PubMed=9628581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        683
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2; Conserv
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18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9; DB 4;
Pred. No. 2.1e-
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Catarrhini; Hominidae; Homo
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                                                                       Α.,
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                                                                       Zhang L., Chan H.M.,
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                                                                                                              Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Patlazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syirskas R., Fector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S. M. Wassarman D.A., Weinstock G.M., Weinschol
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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NCBI_TaxID=7227;
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Science 287:2185-2195(2000).
EMBL; AE003750; AAP56375.1; -
FlyBase; FBgn0039257; CG13648.
InterPro; IPR001007; VWF_C.
Pfam: pe70093; VWC; 1.
SMART; SM00214; VWC; 4.
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Trebouxia jamesii.
Eukaryota; Viridiplantae; C
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Kroken S., Taylor J.W.;

"Phylogenetic species, reproductive mode, and forming lichens with the fungal genus Letharia submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF242472; AAF78028.1; -.
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01-MAY-2000
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                                                                                                                                                                  Q9LL43
                                                                                                                                                                                                                                                                                                              VHL protein
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                                         SEQUENCE FROM N.A. Kroken S., Taylor
                                                                                                              Actin type I (Fragment).
                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                        NCBI_TaxID=53267;
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18.2%;
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                    reproductive mode, and
he fungal genus Letharia
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. 13, Last sequence. 13, Last annotation.
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RESULT 15
Q9NMB
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AC Q9NMB
AC Q9NMB
DT 01-000
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DT 01-000
DE Hypotl
GN LM26...
GN SEQUE
RC STRAIL
RA Murph
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SQ SEQUE
Search completed: January 15, 2003, 12:35:28 Job time: 35.5714 secs
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                                                                                                                                                                    Query Match 44.4%; Score 8; DB 5; Length 60; Best Local Similarity 18.2%; Pred. No. 1.9e-09; Matches 2; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                  STRAIN=FRIEDLIN;
Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL160493; CAB97,792*1; -.
Hypothetical protein.
NON_TER 60 60
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Pfam; pF00022; actin; 1.
NON_TER 1 1
NON_TER 56 56
SEQUENCE 56 AA; 6357 MW; 64F701537B21BD32 CRC64;
                                                                                                                                                                                                                                                              SEQUENCE 60 AA; 6484 MW; 15A5F9C8EC19325C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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-MODEL-frame+_p2n.model -DEV=xlh
-Q=/c9n2_L/USPTQ_spool/US09823649/runat_14012003_151002_29139/app_query.fasta_1.1393
-DB=GenEmbl -QEMT=fastap_SUFFIX=ryg-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pct -NORM=ext -HARASIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER=US09823649_@CGN_1_1_3378_@runat_14012003_151002_29139 -NCPU-6 -ICPU=3
-NO_KIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAXIT -LOONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XOAPOD=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPED=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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36: em_htg_wrt:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_num:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 224)
                                                                                                                                                                                                                                                                                          sequence.
AY022699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto Rice Genome Sequencing project. Please see http://www.rice-research.org for more information. The sequence data were produced primarily in the laboratories of Dr. Leroy Hood at the University of Washington in Seattle.
Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh Blvd., Creve Coeur, MO 63167, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa microsatellite MRG5020 containing (CCG)X8, closest to marker S12158, genomic sequence.

AY022695
                                   Direct Submission
                                                    Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
                                                                                       Unpublished
                                                                                                      Simple sequence repeats from Monsanto rice genomic sequences
                                                                                                                                                                                                                                     Oryza sativa.
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                                                                                                                         Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.
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                                                                                                                                                                                                                                                                            http://www.rice-research.org for more information. data were produced primarily in the laboratories o at the University of Washington in Seattle.
                                                                                                                                                                                                                                                                                                                            Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh Blvd., Creve Coeur, MO 63167, USA Derived from rice genomic sequences generated from the Monsanto Rice Genome Sequencing project. Please see
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                          AY023249 227 bp DNA linear PLN 07-FEB-200: Oryza sativa microsatellite MRG5574 containing (GGA)X9, closest to marker RZ272, genomic sequence.
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Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G.F.
Simple sequence repeats from Monsanto rice genomic sequences
                                                             Oryza sativa.
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                                                                                                                                                       Salt Lake City, UT 84112
                                                                                                                                                                                                        Submitted by:
                                                                                                                                                                                                                          Unpublished (1994)
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                                                                                                                                                                     e-mail: sts@corona.med.utah.edu
Primer A: AGATCGCGCCATTGCACTC
Primer B: TTTCTGGCTACTGCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human STS UT7920, 3' primer bind, sequence tagged site.
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Derived from rice genomic sequences generated from the Monsanto
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Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G
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2160 Eccles Institute of Human Genetics
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AL110710
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cDNA library; nitrogen deprivation
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                                                                                                                                                                                                                                                                                                                                                                                                                         Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
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                                                                  CNS018RJ
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The cDNA library to be analyzed within the framework of this project was created using a Botrytts cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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                                                                                                                                                                      Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Botryotinia fuckeliana
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Botryotinia fuckeliana
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1 (bases 1 to 480)

    Web : www.genoscope.cns.fr)

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/note="Genoscope sequence ID : W30B091"
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/strain="T4"
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Submitted (25-DEC-1999) Lab of Animal Virology, College of Animal Science and Veterinary Medicine, Huazhong Agricultural University, Wuhan, Hubei 430070, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fang, L.R., Xiao, S.B., Xu, J.X., Hong, W.Z. and Chen, H.C. Cloning and expression of IE180 gene of pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 560) Fang, L.R., Xiao, S.B., Xu, J.X., Hong, W.Z. and Chen, H.C.
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/strain="T4"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W24E051"
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/note="Genoscope sequence ID : W24E051"
                                                                                                                                                                    /protein_id="7AF43385.1"
/db_xref="G1:7243655"
/db_xref="G1:7243655"
/translation="MadDLFDFTETEGNESQLLAAAAAAAAAEEEGTAAGSDGGSQGS
/translation="MadDLFDFTETEGNESQLLAAAAGATRPPRPPSAQQQQQQQPRR"
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/db_xref="taxon:10345"
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        Machado, C.A., Kliman, R.M., Markert, J.A. and Hey, J.
Inferring the History of Speciation from Multilocus DNA Sequence
Data: The Case of Drosophila pseudoobscura and Close Relatives
Mol. Biol. Evol. 19 (4), 472-488 (2002)
                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Machado, C.A., Kliman, R.M., Markert, J.A. and Hey, J.
Direct Submission
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="3002 locus"
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/strain="MSH42"
/db_xref="taxon:7234"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                         Mol. Biol 21918426
                                                                                                                                                                                                                                                     Submitted (21-NOV-2001) Department of Genetics, 604 Allison Rd., Piscataway, NJ 08854-8082, USA
                                                                                                                                                                                                                                                                                                                                                 Machado, C.A., Kliman, R.M., Markert, J.A. and Hey, J.
Inferring the History of Speciation from Multilocus INA Sequence
Data: The Case of Drosophila pseudoobscura and Close Relatives
Mol. Biol. Evol. 19 (4), 472-488 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila
AF450791
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                                                                                                                                                                                                                                      604 Allison Rd., Piscataway,
Location/Qualifiers
                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila pseudoobscura
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila pseudoobscura.
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Machado,C.A., Kliman,R.M., Markert,J.A.
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/strain="Flagstaff16"
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/strain="AFC3"
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US-09-823-649A-1 (1-11) x CNS01DLJ (1-636)
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ALI16975
ALI16975 1 GI:5832191
CDNA library - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                      Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota;
Helotiales; Sclerotiniaceae; Lacidates to 660)
                                                                                                                                                                                                                                   CNSOIBJR 660 bp mRNA linear PLN 02-
  Bitton, F., Levis, C., Fortini, D., Pradier, J.M.
                                                                                                               cDNA library; nitrogen deprivation. Botryotinia fuckeliana.
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AL114319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
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and Brygoo, Y.
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BASE COUNT
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
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Direct Submission
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179 c 180 g 148 t
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

07-FEB-2002

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genome-deri	#7175	past nasan	#15764	#11420	5	bone	bone m	brain	brain expre	#12098 for	#10080	foetal	foetal	breast of	_	ide	-	dopsis the	prostate	TO .		nucleotide	genome-der	#101 used	#104 usec	#102	bone marrow	Human brain expres	#07 for	fortal	DI Eds C	n breast	Human breast cance	g nove	acid	c acid	idonic	human pol	uman secreted	lone DM293	secreted	Human spliced tran	cription

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ABN37254
                                                                                                       Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
WO200210449-A2
                                                                                                                                                                                                Human spliced transcript detection oligonucleotide SEQ ID NO:10002
                                                                                                                                                                                                                                                       15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                             ABN37254;
                                                                                                                                                                                                                                                                                                                                                                              ABN37254 standard; DNA; 60 BP.
                                                   Homo sapiens
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RESULT 1

ALIGNMENTS

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RESULT 2
AACO4346/c
ID AACO43
XX AACO43
XX AACO43
XX DF O6-OCT
XX
XX Human;
XX Gene t.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the genome, which encodes one or more messenger RNA splice variants. CC The oligonucleotide libraries are useful for detecting mRNAs from a CC biological sample, in expression profiling studies, in qualitatively or CC quantitatively characterising the corresponding transcriptome, and in CC detecting RNA transcripts and splice variants of human or animal cC transcriptomes. The libraries may also be used as specialised mini CC libraries to detect transcripts of a sub-transcriptome under a particular biological, or pathological state, and so allowing the CC detection of tissue- and pathology-specific genes such as those genes CC only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA CC transcripts and splice variants of a transcriptome of a patient suffering CC oligonucleotide sequences from rats, humans and mice, which are used in CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
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                                                                                                                                                                                                                                                                                                           US-09-823-649A-1 (1-11) x ABN37254 (1-60)
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                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
              Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                 Human secreted protein 5' EST, SEQ ID NO: 8421.
                                                                                                     06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               several oligonucleotides, each capable of hybridising selectively to
set of messenger RNAs transcribed from a given transcription unit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID 10002; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                                                                                                                                      AAC04346;
                                                                                                                                                                      AAC04346 standard; cDNA; 261 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                messenger RNAs that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes oligonucleotide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental-specific genes
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                                                                                                                                                                                                                                         TTAGCAGCAGCAGCAGCAGCGGCATCGGAG 55
                                                                                                   (first entry)
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50.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                              Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                            Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-823-649A-1 (1-11) x AAC04346 (1-261)
                                                                                                                                                                                                                                                                                                         AAV90423/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dT primed cDNA ilbraries. Such ESTs are not well swited for isolating CDNA sequences they ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Parcession and secretars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
15-OCT-1998
                                                                                              gene therapy;
                                                                                                                                Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
                                                                                                                                                                                                                     15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 261 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 8421; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-500381/45
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                                W09845436-A2
                                                                                                                                                                                     EST clone DM293.
                                                                                                                                                                                                                                                        AAV90423;
                                                                                                                                                                                                                                                                                     AAV90423 standard; cDNA; 280 BP
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                                                               Homo sapiens
                                                                                                                    receptor;
                                                                                                                                                                                                                                                                                                                                                        62 THAGCTCCCACAHCCTCTTCCHCTTCCTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                         1 Leuskaakkakkakkkkkkkkkakkakkakkkkkl]u 11
                                                                                                ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
apy; ss.
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                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
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RESULT 4
AAC17532
           ACC XXX ACC XX
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity.
        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy
                                                                                                               26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 536; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, tesles, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                      21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                               99US-0122487
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        Duclert A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lavallie ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 21607
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Matches:
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        Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                          Williams LT,
Reinhard C, R
Crkenjakov R,
WPI; 2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2001
                                                         Kita D,
                                                                                                                                                                                                                                                                          02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000WO-US18374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                       (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                 02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
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Garcia V,

Jones

LW,

Randazzo F,
R, Drmanac S,

Kennedy GC,
Dickson M,

nis MA, Garcia PD, nedy GC, Pot D, Lai ckson M, Labat I, Strache-Crain B;

Lamson G,

J, Kassam A; Drmanac R;

Leshkowitiz Klinger J, 99US-0142310. 99US-0142311.

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US-09-823-649A-1 (1-11) x AAC17532 (1-343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTs derived from CC mRNAs encoding secreted proteins. No ORF has yet been conclusively CC identified within the present sequence. The 5' ESTs were prepared from CC total human RNAs or polyA+ RNAs derived from 30 different Lissues. EST CS sequences usually correspond mainly to the 3' untranslated region (UTR) CC in mRNA because they are often obtained from oligo-dT primed cDNA CC libraries. Such ESTs are not well suited for isolating cDNA sequences CC derived from the 5' ends of mRNAs and even in those cases where longer CC cDNA sequences have been obtained, the full 5' UTR is rarely included. CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be comed to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used to in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design cCC expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5') EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
WO200102568-A2
                                                                                                                                                                                                    09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 343 BP; 73 A; 84 C; 79 G; 106 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 21607; 71pp + CD-ROM; English.
                                            Homo sapiens
                                                                                     breast cancer; lung cancer; cancer detection; ss
                                                                                                        Human; cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                     Novel human polynucleotide, SEQ ID NO: 1755.
                                                                                                                                                                                                                                                 AAF65999;
                                                                                                                                                                                                                                                                                              AAF65999 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                           1 Leu**************************Glu 11
                                                                                                                                                                                                                                                                                                                                                                                      TTAGCAGCAGCAGCAGCAGCAGCACCATCGGAG 50
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                              cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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                  WPI; 2000-571881/53.
                                                                                                                                                                                                                                                                                                                                                                      Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositio treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynuclectides. The probes can be used for chromosome mapping of the polynuclectide and for detection of transcription levels. Ribozymes or antisense oligonuclectides can be generated. The polynuclectides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the
                                                   Blumenfeld M, Bougueleret L,
                                                                                                                                      07-MAY-1999;
                                                                                                                                                                                                                                                        17-AUG-2000.
                                                                                                                                                                                                                                                                                               WO200047771-A2
                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arachidonic acid metabolism related genomic biallelic marker #223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC57589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 BP; 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
                                                                                             (GEST ) GENSET
                                                                                                                                                       12-FEB-1999;
23-MAR-1999;
                                                                                                                                                                                                                   11-FEB-2000; 2000WO-IB00184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC57589 standard; DNA; 362 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carcing jenesis pathway and/or monitor the efficacy of therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 TTAGCAGCAGCAGCAGCAGCATCGGAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 795; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                  99US-0119917.
99US-0275267.
99US-0133200.
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9.00
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                                                         Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                              detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an elcosanoid-related biallelic marker, and for amplifying a marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
                                                                                              12-FEB-1999;
23-MAR-1999;
                                                                                                                                                                                                                WO200047771-A2
                                                                                                                                                                                                                                                                              eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 362 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism - \,
                                                                                                                                               11-FEB-2000; 2000WO-IB00184
                                                                                                                                                                               17-AUG-2000
                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            Human; biallelic marker; arachidonic acid metabolism;
                                                                                                                                                                                                                                                                                                                                                                               Arachidonic
                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC57590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC57590 standard; DNA; 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            base of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention may be used to select individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 422; 802pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 TTAGCAGCAGCAGCAGCAGCAGCATCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes polynucleotides including biallelic
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                              99US-0119917
99US-0275267
                                                                                99US-0133200
                                                                                                                                                                                                                                                                                                                                                                           metabolism related genomic biallelic marker #224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
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WPI; 2000-571881/53 Blumenfeld M,

Bougueleret L,

Chumakov 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                           12-FEB-1999;
23-MAR-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
No.:
                                                                                                                                                                                                                                                                                                                             detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. Anci7367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the
            WPI; 2000-571881/53
                                             Blumenfeld M, Bougueleret
                                                                              (GEST ) GENSET.
                                                                                                                                                                             11-FEB-2000; 2000WO-IB00184
                                                                                                                                                                                                              17-AUG-2000
                                                                                                                                                                                                                                               WO200047771-A2
                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                               elcosanoid-related biallelic marker; 12-10-related biallelic marker; ds
                                                                                                                                                                                                                                                                                                                                                                                                               Arachidonic acid metabolism related genomic biallelic marker #225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC57591 standard; DNA; 362 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNPs) in the polynucleotide sequences from the present invention have been c ver as their corresponding degenerate bases e.g. a polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention. N.B. Polymorphic bases (single nucleotide polymorphisms also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplification assays for identifying an elcosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   base of C or T has been given as Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leu*****************************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAGCAGCAGCAGCWGCAGCRGCATCGGAG
                                                                                                                                                                                                                                                                                                                                                                                biallelic marker; arachidonic acid metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                           99US-0119917.
99US-0275267.
99US-0133200.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amplification assays for identifying an eicosanoid-related biallelic marker (BRBM) or 12\text{-}10\text{-}\text{related} biallelic marker, and for amplifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -       
                                                                      P-PSDB; ABG20360.
                                                                                     WPI; 2001-639362/73
                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #20351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS84547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS84547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 362 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNPs) in the polynucleotide sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes polynucleotides including biallelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 423; 802pp; English
                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                     food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 TTAGCAGCAGCAGCAGCAGCAGCATCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Leu**************************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given as their corresponding degenerate bases e.g. a polymorphic of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 436 BP
                                                                                                                                                                                    2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T has been given
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                c mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                   Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
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RESULT 10
AAL17892
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XX AAL17
XX O7-DE
XX Human
XX Human
XX Homo
XX Homo
XX 19-JU
XX 19-JU
XX 12-JA
PR 14-MA
PR 29-MA
PR 29-MA
PR 15-MA
PR 15-MA
PR 15-MA
PR 29-JU
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XX 11-JA
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Query Match:
DB:
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                                                                                                                                                    14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in
                                                                                                                  29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                        10-JAN-2001; 2001WO-US00798.
                                                                                                                                                                                                                                                               19-JUL-2001
                                                                                                                                                                                                                                                                                                 WO200151628-A2
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer expressed polynucleotide 10349.
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL17892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL17892 standard; cDNA; 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 20351; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to isolated polynucleotide (I) and ypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTCATCCTCTTCCTCCTCATCATCAGAG
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                                                                                                  ; 2000US-0176077.
; 2000US-0189167.
; 2000US-0192099.
; 2000US-0193480.
; 2000US-0205230.
; 2000US-0211315.
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                                                                                   2000US-0220534.
            Y,
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            Wang Y,
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              Steinmann K;
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Matches:
Conservative:
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Best Local Similarity:
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                                                                                                                                                                                                                                                    24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
                                                       Claim 1; Page 1867; 3695pp; English.
                                                                                        New peptide useful as a marker for the
                                                                                                                              WPI; 2001-451856/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human breast cancer expressed polynucleotide 10450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL17993 standard;
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                                                                                                                                                                 Lillie J,
                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                     25-JUL-2000;
                                                                                                                                                                                                                                                                                                                            14-JAN-2000; 2000US-0176077
14-MAR-2000; 2000US-0189167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polynucleotides and encoded polypeptides are potential markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451856/48
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                                                                                                                                                                 Xu Y,
                                                                                                                                                                                                                                                                                         ; 2000US-0189167.
; 2000US-0192099.
; 2000US-0193480.
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                                                                                                                                                                                                                                     2000US-0220534
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2000US-0211315.
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                                                                                                                                                               Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; 437
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                                                                                                                                                               Steinmann K;
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                                                                                        diagnosis of breast cancer
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RASUUT 12

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ID AALO9

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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                          The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                       The invention relates to human breast cancer expressed polynucleotides (AALO7544-AALI26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
                                                                                                                                                                                                                                          Claim 1; Page 412;
                                                                                                                                                                                                                                                                                                                                                               Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200151628-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001.
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                                                                                                                                                                                                                                                                                 peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                         2001-451856/48
                                                                                                                                                                                                                                                                                                                                                               Xu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0176077.
; 2000US-0189167.
; 2000US-0192099.
; 2000US-0193480.
; 2000US-0205230.
; 2000US-021315.
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                                                                                                                                                                                                                                        3695pp; English.
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Alignment Scores:

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Best Local Similarity:

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Matches: Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                      29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
                                            expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                           The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the
                                                                                                                                               Claim 1; Page 604; 3695pp; English.
                                                                                                                                                                      New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                           14-MAR-2000;
24-MAR-2000;
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                       polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                                                                                           Lillie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human breast cancer expressed polynucleotide 3276.
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                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 CTGACAGCAGCAGCCTCTTCCACATCAAGTGAA 115
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2000US-0192099.
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XX O4-FEB
PR 04-FEB
PR 03-AUG
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                           Sequence 462 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing
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                                                           288 CTGACAGCAGCCTCTTCCACATCAAGTGAA 256
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                                                                                                   SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetal liver; gene expression; single exon nucleic acid probe;
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascues. e.g. cardiovascular disease, hypertension, cardiac arrhythmias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 462 BP; 131 A; 124 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human hearts -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital heart disease.
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                                                                                                                                                                                                   (1-462)
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Sequence Sequence Sequence

876, App
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49, Appl
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107, App
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144, Appl
151, Appl
164, Appl
165, Appl
242, App

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Result
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-MODEL-frame+_D2n.model -DEV=xlh
-Q-/cgn2_1/USSPO_Spool/USS9823849/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB=Issued_Patents_Na -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -SYRAFI=1 -END=-1 -MAYRIX=blosum62 -TRANS=hunan40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN-2000000000
-USER-USO9823649 -GCQN_1_1_35_etunat_14012003_151002_29127 -NOPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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    nucleic search, using frame_plus_p2n mode.

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      length: 20000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
                                                                                                                                                                        Match
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                                                                                                                                                                                       Query
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
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/cgn2_6/ptodata/1/ina/6A_COMB.seq: *
/cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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US-09-068-051A-23

US-08-959-011-2

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Sequence 877, App
Sequence 878, App
Sequence 223, App
Sequence 225, App
Sequence 225, App
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 68, Appl
Sequence 33, Appl
                                                                                                                                                                        Description
                                       : OTHER INFORMATION: 10-87-74 : polymorphic base US-09-641-638-877
                                                                                                                                                                               CUMRENT APPLICATION NUMBER: US/09/041.638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
               Alignment Scores:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 877, Appl Patent No. 6432648
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGION THILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENESET 0570-1
                                                                                                                                                                      PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                               NAME/KEY: allele
LOCATION: 24
                                                                                                     ORGANISM: Homo Sapiens
                                                                                                                   TYPE: DNA
                                                                                            FEATURE:
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US-08-67-613-107
PCT-USS-09816A-107
US-08-207-481-4
PCT-USS-02689-51
US-08-594-031-14
US-08-594-031-14
US-09-641-638-22
US-09-199-637A-242
US-09-199-637A-242
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US-09-128-155-3

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US-09-199-637A-240

US-09-219-625-1

US-08-207-481-25

PCT-US95-02689-25

US-09-222-939-24

US-09-128-155-1

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PCT-US95-02689-40
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US-08-737-524B-18
US-08-823-771-94
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Sequence Sequence Sequence Sequence

38, Appl 40, Appl , Appli 1, Appli

Sequence

10, Appl 32, Appl 6, Appl 6, Appl 10, Appl 207, Appl 21, Appl 25, Appl 25, Appl 24, Appl 25, Appl 24, Appl 27, Appl

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                                                                                                                          GENERAL INFORMATION: APPLICANT: Blumenf
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLIANG DATE: 2000-08-16
                                                                                                                                                             Sequence 223, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Pa
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-03-23
                                                                      APPLICANT:
                                                                                                         APPLICANT:
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
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                                                                                       Bougueleret, Lydie
Chumakov, Ilya
                                                                                                                            Blumenfeld, Marta
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Conservative:
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US-09-641-638-224
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PRIOR APPLICATION NUMBER: US 60, PRIOR APPLICATION NUMBER: US 60, PRIOR APPLICATION NUMBER: US 69, PRIOR FILING DATE: 1999-03-23, PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                       Sequence 224, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 223
                                     PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-1
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/641,638 CURRENT FILING DATE: 2000-08-16
                                                                                                                                                                TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEET.051CP1
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SOFTWARE: Patent.pm
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PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_binding LOCATION: 74..93 OTHER INFORMATION: 10-87-74.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_binding
LOCATION: 53..72
OTHER INFORMATION: 10-87-74.misl, potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 10-87-74 potential probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 73
OTHER INFORMATION: 10-87-74 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele LOCATION: 73
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Chumakov, Ilya
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BER: US 09/502,330
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US-09-823-649A-1 (1-11) x US-09-641-638-224 (1-362)
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                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 225
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SEQ ID NO 224
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                                                                                                                                                                                                                                          PRIOR EILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 6
PRIOR EILING DATE: 1999-05-07
PRIOR APPLICATION OF THE PRIOR
                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: GENSET.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC RECIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/119,917 PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                            PRIOR FILING DATE:
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            TYPE: DNA
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LOCATION: 59..78
OTHER INFORMATION: 10-87-80.mis1, potential
NAME/KEY: misc_binding
LOCATION: 80..99
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ORGANISM: Homo Sapiens
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LOCATION: 345..362
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Chumakov, Ilya
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Best Local Similarity:
Query Match:
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US-08-597-495B-23
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APPLICANT: Old, Lit
APPLICANT: Simpson
APPLICANT: Catimel
APPLICANT: Heath,
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OTHER INFORMATION: 10-87-140 potential probe
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LOCATION: 118..137
OTHER INFORMATION: 10-87-140.mis1, potential
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OTHER INFORMATION: 10-87-140 : polymorphic base C or T
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                              APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5712369man D
                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                          PRIOR APPLICATION DATA:
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NAME: Hanson, No. 5 REGISTRATION NUMBER:
                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 02-Feb-1996
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: F
                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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I: 805 Third Avenue
New York City
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Indels:
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GENERAL INFORMATION:
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TELEPHONE: (212) 688-9200
TELEPAS: (212) 838-3884
INFORMATION FOR SEQ ID NO: 23:
                                                                                                          TELEPHONE: (212) 318-3168
TELEPAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard, Moritz, R. L.;
Catimel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
SEQUENCE DESCRIPTION: SEQ ID NO: 23
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LUD 5316.2 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                      LENGTH: 960 nucleotides TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                   NAME: Hanson, No. 6291235man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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Best Local Similarity:
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Best Local Similarity:
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                                                                      Pred. No.:
                                                                                    Alignment Scores:
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APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                             TOPOLOGY: linea IMMEDIATE SOURCE: LIBRARY: CRBLNC CLONE: 676592
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APPLICATION NUMBER: US
FILING DATE: Herewith
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APPLICANT: Shah, Purvi
APPLICANT: COrley, Neil C.
TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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OPERATING SYSTEM: DOS
SOFTWARE: FASTENO for Windows Version
                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                  STRANDEDNESS: single
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Conservative:
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Indels:
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Indels:
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US-09-823-649A-1 (1-11) x US-08-959-011-2 (1-2156)

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US-09-068-051A-31
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Best Local Similarity:
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                                                                                                                   Patent No. 6291235
GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 31, Application US/09068051A
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LENGTH: 2565 nucleotides
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APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;
APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              867 TTGGCATCATCTACTGCTGCTGCCGAG 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/597,495B FILING DATE: 02-Feb-1996 CLASSIFICATION: 435. *
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OPERATING SYSTEM: PC-
SOFTWARE: Wordperfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/511,876
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APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd; Simpson, Richard J.; Nice, Edouard; Moritz, R. I..; Catimel, B.; Ji, Hong; Burgess, Anthony W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leu**********************************Glu
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805 Third Avenue
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US-09-336-536-68
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Query Match:
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; Sequence 68, Appiium

; Sequence 68, App
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                                                                            SEQ ID NO 68
LENGTH: 2793
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 318-318
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 31
                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
CORRESPONDENCE ADDRESS:
                                          NUMBER OF SEQUENCES:
```

STREET: 666 Fifth Avenue ADDRESSEE: Fulbright & Jaworski LLP

COUNTRY: USA STATE: New York CITY: New York City

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2

CURRENT APPLICATION DATA: OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect APPLICATION NUMBER: US/09/068,051A

PRIOR APPLICATION DATA FILING DATE: 10-Dec-1998 CLASSIFICATION: 435

APPLICATION NUMBER: 08/511,876 FILING DATE: 04-Aug-1995 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 08/597,495 FILING DATE: 02-Feb-1996

TELECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: LUD 5316.2 318-3168

SEQUENCE CHARACTERISTICS: LENGTH: 2565 nucleotides

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: US-09-068-051A-31 3

18.18% 18.18% 50.00% 189 Length: Matches: Caps: Conservative: Mismatches: indels:

US-09-823-649A-1 (1-11) x US-09-068-051A-31 (1-2565)

1 Leu\*Glu 11

867 TTGGCATCATCTACTGCTGCTGCTGCCGAG 899

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: MCKBy, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF, FILE REFERENCE: 7853-144 Application US/09336536

SOFTWARE: PatentIn Ver. 2.0

US-09-336-536-68

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Query Match:
                                                             Best Local Similarity:
                                                                                Percent Similarity:
                                                                                                                   Pred. No.:
                                                                                                                                    Alignment Scores:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 33:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/597,495
FILING DAFE: 02-Fcb-1996
APPLICATION NUMBER: 08/511,876
FILING DAFE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Catimel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS SOFTWARE: WORDERFECT CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2803 nucleotides
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ADDRESSEE: Fulbright & Jaworski LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               NAME: Hanson, No. 6291235man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 5316.2
                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 666 Fifth Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 318-31
TELEFAX: (212) 752-5958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
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Matches:
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                                                             Mismatches:
                                            Indels:
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US-08-737-524B-18
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Best Local Similarity:
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US-08-474-633A-94
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                Sequence 18, Application US/08737524B Patent No. 5912414 CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94, Application US/084746334 Patent No. 5773691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: E. I. DU
APPLICANT: COMPANY
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDJIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICANT: CARL SAVERIO FALCO
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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CITY: WILMINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                          1 CTAGAAGCCTCGGCAACGTCAGCAACGGCGGAA 33
                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND THREONINE CONTENT
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                                                                                                                                                                                                     Sequence 94, Application US/08823771
Patent No. 6499019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE N
COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS*
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 302-992-54
TELEPAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                               1 CTAGAAGCCTCGGCAACGTCACCAACGGCGGAA 33
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       TITLE OF INVENTION: CHIMERIC GENES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19898
CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A.
                                                  AND COMPANY
STREET: 1007 MARKET STREET
                                                                                    ADDRESSEE: E. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             835420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMINICK ANTHONY GUIDA, JR. MARY ELIZABETH HARNETT LOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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GENES AND METHODS FOR INCREASING
THE METHIONINE CONTENT OF THE SEEDS
OF PLANTS
                                                                                                                                                                                                                         DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                     METHODS FOR INCREASING INCREASING THE LYSINE
                                                                                                                                      AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18:
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                                                                                    DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB-1059-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
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Qy
                                                                                                                                     US-09-823-649A-1 (1-11) x US-08-823-771-94 (1-43)
Search completed: January 15, 2003, 12:58:36 Job time: 30 secs
                                                                      дb
                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                            US-08-823-771-94
                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 835420
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                     1 Leu***************************Glu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: LBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/474,633 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MICROSOFT WORD VERSION 2.0C CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                  CTAGAAGCCTCGGCAACGTCAGCAACGGCGGAA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/823,771 FILING DATE: 24-Mar-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BARBARA C. SIEGELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 302-992-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302-773-0164
                                                                                                                                                                                              18.18%
18.18%
44.44%
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8.00
                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                  Conservative:
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Result
No.
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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
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                                                                                                                                                                                                                                     Query
Match
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    93.666666
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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT: *

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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: *

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: *

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT: *

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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: *

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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseg/genesegp-embl/AA1983.DAT:*
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                                                                                                                                                                                                                                        DB
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                                         AAM48262
AAM48263
AAM48264
                                                                                                       AAB47793
AAB47794
AAM48259
AAM48260
AAM48261
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(without alignments)
52.083 Million cell updates/sec .
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AAR23154		316	AAR23161	AAR23155	14	AAE15569	AAE15568	AAE15565	AAR23167	AAR23162	AAR23156	AAR23144	AAU00575	AAU00574	AAR96204	AAR99543	AAE09310	AAE09305	AAY00887	AAW09316	AAY00888	AAY00886	AAW09317	AAW09315	AAR96205	AAR99544	AAY44353	AAR66209	AAY44352	AAE09304	AAR23157	316	AAR23163	AAR23145
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## ALIGNMENTS

RESULT 1
AAB47793
ID AAB4
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AC AAB4
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DT 25-)
XX
KW DN/
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XX
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OS Th
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PD 0
XXX
PF 0
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PF 1
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XX
PT
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PT Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture WPI; 2002-076891/11. Smith ES, Elfstrom CM, Ge. Schoenbrunner NJ, Wang AM; 12-APR-2001; 2001EP-0109341 07-NOV-2001 EP1152062-A2 Thermus sp. 18-APR-2000; 2000US-198336P (HOFF ) HOFFMANN LA ROCHE & CO AG Gelfand DH, Higuchi RG, Myers TW;

dye; amplification.

Native DNA polymerase motif #3

AAB47793;

25-MAR-2002

(first entry)

AAB47793 standard; peptide; 11 AA

DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;

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US-08-180-524-8
US-08-180-524-8
Sequence 8, Application US/08180524
; Patent No. 5849537
; Patent No. 5849537
                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudopleuronectus americanus US-08-180-524-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 66-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acide STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS
                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
                                                                                                               APPLICANT:
                                                                                                                            APPLICANT:
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STREET: 411 Eas
CITY: Milwaukee
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APPLICATION NUMBER:
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CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 18.2 les 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                     1 LXXXXXXXXX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Thad Kryshak, Quarles & Brady
411 East Wisconsin Avenue
                                                              Chicoye, Etzer
Barney, Michael C.
Bower, Patricia A.
Cronan, Charles L.
Cronan, Charles L.
NVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
NVENTION: IN YEAST
               E: Thad Kryshak, Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                       Rhodes, Thomas
Huige, Nick
                                                                                                                                                                                                                         Tripp, Matthew
Lusk, Lance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 2; I
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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; MOLECULE TYPE: I
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-180-524-8
                                            Query Match
Best Local Similarity
Watches 2; Conserve
 밁
                                                                                                                                                                                                                                                                  TELEFAX: (414) 277-55
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
NFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
12 LTAANAKAAAE 22
                                                                                                                                                                                                        LENGTH: 3/ um...
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/409,217 FILING DATE: 19-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Wisconsin
                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             NAME: Kryshak, Thad REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                        TOPOLOGY:
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18.2%;
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                                                                         Score 7;
Pred. No.
                                                            Mismatches
                                                                                       DB 2;
                                                                           4.5e+02;
                                                                                       Length 37;
                                                           Indels
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Search completed: January 15, 2003, 12:38:20 Job time: 11.2857 secs

0; Gaps

0;

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/P

2: /cgn2_6/ptodata/2/pubpaa/U

3: /cgn2_6/ptodata/2/pubpaa/U

4: /cgn2_6/ptodata/2/pubpaa/U

6: /cgn2_6/ptodata/2/pubpaa/U

5: /cgn2_6/ptodata/2/pubpaa/U

6: /cgn2_6/ptodata/2/pubpaa/U

7: /cgn2_6/ptodata/2/pubpaa/U

9: /cgn2_6/ptodata/2/pubpaa/U

10: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U

11: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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18
1 LXXXXXXXXX 11
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               January 15, 2003, 11:20:34; Search time 10.8571 Seconds (without alignments) 20.140 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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   10 US-09-788-963-2

10 US-09-925-301-1264

9 US-10-047-542-87

10 US-09-864-761-33469

10 US-09-858-718-6

10 US-09-784-877-1599

9 US-09-738-626-4316

9 US-09-738-626-6186
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10
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9 US-10-095-407-7

9 US-10-095-528-25

9 US-10-095-407-2

9 US-10-139-833-11

9 US-10-139-833-13

9 US-10-63-547-142

10 US-09-788-963-6397

10 US-09-788-963-6397

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                             Sequence 25, Appli
Sequence 27, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 142, Appli
Sequence 142, Appli
Sequence 6397, Appli
Sequence 6397, Appli
Sequence 1264, Appli
Sequence 1264, Appli
Sequence 87, Appli
Sequence 6, Appli
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Sequence 7, Appli
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Best Local
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	10	10	12	10	10	9	10	10	10	10	9	9	12	9	9	10	2	10	10	9	10	9	10	10	ڡ	9
	US-09-858-754-3	US-09-764-176-7	US-10-000-864-2	US-09-858-754-5	US-09-745-763-140	us-09-738-626-5307	US-09-826-752-4	US-09-858-754-2	US-09-881-752A-144	US-09-852-118-2	US-10-138-713-2	US-09-738-626-6657	US-10-071-751-30	US-10-108-605-51	US-09-738-626-5097	US-09-826-752-14	US-10-115-406-4	US-09-815-242-11250	US-09-866-562-62	US-09-738-626-6416	US-09-858-718-4	US-09-938-269-1	US-09-858-664A-16	US-09-811-284-140	US-09-738-626-3880	US-09-989-919-84
:	. س	7,	N	51 20	Sequence 140, App	Sequence 5307, Ap	4	Sequence 2, Appli	Sequence 144, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 6657, Ap	Sequence 30, Appl	Sequence 51, Appl	5097	14	Sequence 4, Appli	Sequence 11250, A	Sequence 62, Appl		Sequence 4, Appli	Sequence 1, Appli	Sequence 16, Appl	•	3880	Sequence 84, Appl

## ALIGNMENTS

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RESULT 2
US-10-095-407-7
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Sequence 7, Application US/10095407
Patent No. US20020164330A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 11
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Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/095,407 CURRENT FILING DATE: 2002-03-11 PRIOR APPLICATION NUMBER: US 60/091,650 PRIOR FILING DATE: 1998-07-02 PRIOR APPLICATION NUMBER: US 60/054,646 PRIOR FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                          44.48; Local Similarity 18.28; hes 2; Conservative
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 Mismatches

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Query Match
Best Local Similarity
""trhes 2; Conserve
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PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                      US-10-095-407-2
                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 4365383CD1
US-09-965-528-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-407-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-965-528-25
   Sequence 2, Application US/10095407 Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 176
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APPLICANT: INCYTE G
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/146,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PF-0701 USA
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                          52 LASSISSASAE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LASSLSSASAE 53
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                                                                                                                                             1 LXXXXXXXXX 11
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BANDMAN, Olga *
BAUGHN, Mariah R.
AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANG, Y. Tom
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18.28;
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                                                                                                                                                                                             Score 8;
Pred. No.
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Pred. No.
                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                               DB 9;
51;
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50;
                                                                                                                                                                                                              Length 176;
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RESULT 6
US-10-139-833-13
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                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Homo sapiens US-10-139-833-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                  Matches
                                                                                                                                                                                                                                                   SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 18.28;
Matches 2; Conservative
                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION UNMHER: 60/195,910
PRIOR FILING DATE: 2000-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Saris, Christiaan M. APPLICANT: Giles, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 37 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TYPE: PRT
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                    54 LASSISSASAE 64
                                                                                              Local Similarity les 2; Conserv
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                                                          1 LXXXXXXXXX 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bass, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mu, Sharon X.
                                                                                                Conservative
                                                                                                              44.48;
18.28;
                                                                                              0
                                                                                                              Score 8;
Pred. No.
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Pred. No. 51;
                                                                                              Mismatches
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                                                                                                                DB
51;
                                                                                                                                9;
                                                                                                                              Length 178,
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; TYPE: PRT; ORGANISM: Homo Sapien US-10-063-547-142
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                           Query Match 44.4%;
Best Local Similarity 18.2%;
Matches 2; Conservative
                                                                                                                                                                        SEQ ID NO 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 142, Application US/10063547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No.
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CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                       Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
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TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
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                                                                                                                                                                                                                                                                 FILE REFERENCE: P3230R1C1
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PRIOR FILING DATE: 2000-11-28
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PRIOR FILING DATE: 2000-04-10
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VRIOR APPLICATION NUMBER: 60/
VRIOR FILING DATE: 2000-04-04
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PRIOR FILING DATE: 1999-12-10
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URRENT FILING DATE: 2002-05-06
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Gerritsen, Mary E.
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CURRENT FILING DATE: 2001-12-06
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              APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
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FILING DATE: 1998-10-08
APPLICATION NUMBER: 60/105000
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APPLICATION NUMBER: 60/108807
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APPLICATION NUMBER: 60/101738
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FILING DATE: 1998-09-22
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APPLICATION NUMBER: 60/100683
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APPLICATION NUMBER: 60/100662
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APPLICATION NUMBER: 60/099812
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FILING DATE: 1999-08-25
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FILING DATE: 1998-12-16
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Similarity 18.2
2; Conservative
                                                NUMBER: 09/380142
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RESULT 9 US-09-788-963-6 ; Sequence 6, Application US/09788963

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RESULT 11
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US-09-738-626-6397
                                                                                                                                     Query Match 44.4%; Score 8; DB 9; Best Local Similarity 18.2%; Pred. No. 55; Matches 2; Conservative 0; Mismatches
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6397
LENGTH: 206
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Best Local Similarity 18.2%;
Matches 2; Conservative
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SEQ ID NO 6
LENGTH: 198
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CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/452,140
PRIOR FILING DATE: 1999-12-01
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APPLICANT: MCDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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Query Match
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Watches 2; Conserve
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US-09-788-963-2
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CURRENT FILING DATE: 2001-02-20
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TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
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PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
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PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
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                                                                                                                                                         TYPE: PRT
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                                     Conservative
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                                                      44.48;
18.28;
                                 Score 8; DB 10; Length 218; Pred. No. 56; 0; Mismatches 9; Indels
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Pred. No. 56;
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RESULT 13

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Query Match
Best Local Similarity 18.2.
Watches 2; Conservative
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US-09-864-761-35469; Sequence 35469, Application US/09864761
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                                      RESULT 15
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; SEQ ID NO 87
; LENGTH: 917
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1264, Application US/09925301
Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/047,542 CURRENT FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AND BACTERIAL DISEASES FILE REFERENCE: 030905.0004.CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL TITLE OF INVENTION: AND BACTERIAL DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LARRICK, JAMES W. APPLICANT: WYCOFF, KEITH L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,301
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE RETERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/200,298
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                             282 LVATATATASE 292
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18.28;
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Pred. No.
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Pred. No.
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Best Local
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                OTHER INFORMATION: KXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELATO, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELATO, SIGNAL = 0.98
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PRIOR APPLICATION NUMBER: PCT/US01/00669
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40 LRAAAQTSSAE 50
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                                                                                                      Conservative
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Pred. No.
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Search completed: January 15, 2003, 12:39:50 Job time: 11.8571 secs

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US-09-823-649A-1
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Listing first 45 summaries
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T04681
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C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
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R; Bevan, M.; Rose,
                                                                                        A; Molecule type: DNA
A; Residues: 1-321 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Protein
                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                   A84792
          Query Match
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## ALIGNMENTS

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                                                                          C;Genetics:
A;Gene: At2937380
A;Map position: 2
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g39370
                                                                                                                                                                                                                                                                                                                                                                  A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197 A; Accession: A84792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Accession: A84792
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A; Cross-references: EMBL: AL031135
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A; Accession: T04681
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A; Introns: 33/3; 129/1; 141/3; 179/2; 228/3; 274/3
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                                                                                                                                                                                                                                      A;Cross-references: GB:AE002093; NID:g4056491; PIDN:AAC98057.1; GSPDB:GN00139
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Best Local Similarity 18.2%;
Matches 2; Conscrvative
   Best Local Similarity
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   18.2%;
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                                   Score 9;
       Pred. No. 5.4e-11;
                                   DB 2; Length 321;
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N;Alternate names: morphogenetic protein
c;Species: pisolithus tinctorius
C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 18-Jul-2001
C;Accession: JC4607; PC4145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tagu, D.; Nasse, B.; Martin, F. Gene 168, 93-97, 1996
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A; Note: KIAA0540
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1113 < NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 11-Jan-2002
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A; Accession: T04686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
C;Accession: T04686
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: cultivar Columbia; BAC clone F4B14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-463 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
A; Title: Cloning and characterization of hydrophobins encoding cDNAs from the ectomycord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDHJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Nagase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T00271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein KIAA0540 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                hydrophobin 1 precursor - Pisolithus tinctorius
                                                                                                                                                      JC4607
                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AB011112; NID:d1185382; PIDN:BAA25466.1
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les 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, II.; Nomura, N.; Ohara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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18.2%;
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18.2%;
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A; Residues: 1-140 <TA
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                  A; Experimental source:
                                                     A; Molecule type: mRNA
A; Residues: 1-181 <HES>
                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                               A; Reference number: Z15411
A; Accession: T05925
                                                                                                                                                                       Plant Sci.
                                                                                                                                                                                        R; Hess,
                                                                                                                                                                                                          C; Accession: T05925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain R1
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A; Residues: 1-169 <WHJ>
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les 2; Conservative
                                                                                                                                                                                        W.R.; Gol
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                                                                                                                                                                       133, 191-201,
                                                                                                                                                                                                                                               Hordeum vulgare (barley)
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              cv. Haisa,
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, M.; Shen, M.; Vamathevan, J.J., Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A:Cross-references: EMBL:AJ222779; NID:e1203989; PIDN:CAA10984.1; PID:e1203990
                                                                                                                                                                                                                                              A; Title: Analysis of randomly selcelted cDNAs reveals the expression of stress- and d
                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE001924; GB: AE000513; NID: g6458372; PIDN: AAF10255.1; PID: g645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: C97562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <KUR>
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                             Вb
                                                                                  QY
                                                                                                                                                                                                                    C; Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                                                                                                                             A; Map
                                                                                                                                                                                                                                                             A; Gene: ppiB
                                                                                                                                                                                                                                                                                                         A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE008688; PIDN: AAL42680.1; PID: g17740114; GSPDB: GN00186
                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           science 294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 1 erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.: Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: AB2783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: AGR_C_3090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE007869; PIDN:AAK87452.1; PID:g15156770; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidyl prolyl cis-trans isomerase (AF203881) [imported] - Agrobacterium tumefaciens ($
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                           A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: AB2577; PMID:11743193
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                                                                                                                                                                             Query Match
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                                             17 LAASTFASAAE 27
                                                                                                                             Local Similarity les 2; Conserv
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nes 2; Conserv
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les 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.; Romero, P.; Zhang, S.
294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LXXXXXXXXX 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
                                                                                                                                                                                                                                                                                                                                                                      type: DNA
                                                                                                                                                                                                                                                                                                                                                -189 <KUR>
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18.2%;
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Pred. No.
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                                                                                                                             9; Indels
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A; Experimental source: strain Bristol N2; clone K03E6
                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics
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Query Match
Best Local Similarity
"~+~hes 2; Conserve
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C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87370
A;Status: preliminary
                                                                                                                                                                                                                                                                              homeobox and LIM domain protein lim-6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Mar-2000
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A; Accession: S46760
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Nierman, W.C.; Feldbl: B.; Laub, M.T.; DeBoy,
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                             A; Reference number: Z21506
A; Accession: T34326
                                                                                                                                                                                             R;Latreille, P.; Gattung, S. submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 8R
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A; cross-references:
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A;Cross-references: EMBL:U55375; PIDN:AAC69042.1; GSPDB:GN00028; CESP:K03E6.1
                                A; Residues: 1-334 <LAT>
                                                        A; Molecule type: DNA
                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                   A; Description: The sequence of C. elegans cosmid K03E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U10397; NID:g500647; PID:g500656; GSPDB:GN00008; MIPS:YHR143
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Matches 2; Conserv
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Reldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, Feldblyum, T.V.; Paulsen, I.T.; Ko
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Pred. No. 4e-07;
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Pred. No.
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C; Genetics:

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A; Introns: 15//3; 34. C; Superfamily: actin
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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C;Superfamily: homeotic protein mec-3; homeobox homology; LIM metal-binding repeat homo.
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                 A; Residues: 1-375 <WIL>
A; Cross-references: EMBL: Z83241; PIDN: CAB05817.1; GSPDB: GN00021; CESP: T25C8.2
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A;Accession: T25272
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R;Gardner, A.
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A; Residues: 1-336 < KAW>
A; Cross references: DDBJ; AP000061; NID: g5104821; PIDN: BAA80406.1; PID: g5105092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takakawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
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                                                                                                                                                                                                                              A; Gene: CESP:T25C8.2
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: APE1409
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 Mismatches

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227 LAAAASSSSLE 237
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A; Accession: D97521
A; Status: preliminary A; Map position: circular chromosome C; Superfamily: aspartate transaminase A;Cross-references: GB:AE007869; PIDN:AAK87125.1; PID:g15156389; GSPDB:CN00169 C:Genetics: R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001 probable aspartate transaminase (EC 2.6.1.1) aspB (similarity) [imported] - Agrobacte C;Species: Agrobacterium tumefaciens C;Late: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002 C;Accession: D97521 C; Keywords: aminotransferase A;Gene: AGR\_C\_2460 A; Molecule type: DNA A; Residues: 1-387 < KUR> A; Reference number: A97359; PMID:11743194 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium Query Match Local Similarity hes 2; Conserv 44.48; 18.28; Pred. No. 4.3e-07; Score 8; DB 2; Length 387

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Job time : 20.1429 secs Search completed: January 15, 2003, 12:37:06

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YHU3_YEAST
RRN4_YEAST
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YM8G_YEAST
E412_MUUSE
E412_HUMAN
ALAB_ARATH
MOZ_HUMAN
SEN1_YEAST
WEN2_HUMAN
ANPA_PSEAM
Y507_METTH
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een	-!- TISSUE SPECIFI	-i- SUBCELLULAR LO		-i- CATALYTIC ACTI		-!- FUNCTION: VACU	ubmitted (AUG-200	NEDO human cDNA sequencing protec	uzuki Y., obayash akamura V Tsoga	atanabe K., Kumaga	UENCE		portion using microcione p Genomics 20:404-411/1994)	Isolation of expr	okoi H., Hadano S	MEDLINE=94307726; PubMed=8034313;	TISSUE=Brain:	STOTENCE OF 97-470 FROM N A	Hum. Mol. Genet. 5:659-668(1996).	GGPD loci.";	andidate genes in	"Long-range seguen	uo L., Helmer C.,	Chen E.Y., Zollo M	MEDLINE-96311563; PubMed-8733135;	SEQUENCE FROM N.A.		NCBI TavID=9606:	Eukaryota; Metazoa; Chordata;	Homo sapiens (Human).	ÀTP6IPÍ OR ATP6S1 OR VATPS1	(XAP-3).	Vacuolar ATF Synthase subunit) (V-ATPase Si	15-JUN-2002 (Rel. 41,	16-OCT-2001 (Rel. 4		AN	
	TISSUE SPECIFICITY: UBIQUITOUS.	SUBCEALULAR LOCATION: INTEGRAL MEMBrane protein.	SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.	CATALYTIC ACTIVITY: ATP + $H(2)O + H(+)(In) = H(+)(On+)$	AR COMPARTMENTS IN	OLAR ATPASE IS RES	0) to the EMBL/Geni	"NEDO human cDNA sequencing project.":	Suzuki Y., Obayashi M., Nishi Y., Shibahara Y., Nakamura V Tsocrai M. Sucano S.,	ai A., Itakura S.,	OF 128-470 FROM N.A.	*	ocione probes gene: 1/1994)	essed sequences en	Yokoi H., Hadano S., Kogi M., Kang X., Wakasa K.,	PubMed=8034313;	FROM M.D.	A N MOAA	:659-668(1996).		in 219.4 kb of high GC	"Tong-range segmence analysis in Yg28:	Burough F.W., Ripe	Zollo M., Mazzarella R.A., Ciccodicola A.,	PubMed=8733135;			FI Thid CES;	Chordata;		OR VATPS1 OR XAP3.			11, Last annotation update)	<ol> <li>Created)</li> <li>Last sequence update</li> </ol>		STANDARD: PRT:	
It is produced through a collaboration informatics and the EMBL outstation -		embrane protein. Vacuolar (By		+ H(+)(In) = ADP + phosphate +	OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS (BY SIMILARITY).	FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.		Lbahara T., Tanaka T.,				portion using microcione probes generated by laser microdissection."; Genomics 20:404-411/1994)	"Isolation of expressed sequences encoded by the human Xq terminal	., Wakasa K., Ikeda J.;						3C DNA between the RCP/GCP and	3. thirteen known and six	ZUO L. Heiner C., Burough F.W., Ripetto M., Schlessinger D.,	Ciccodicola A., Chen CN.,				IIII; HOMILIII (de; HOMO.	Craniata; Vertebrata; Euteleostomi;			acceptable fraction ( strange men acceptable)	Subunit St precursor (EC 3.6.3.14) (V-ATPASE St accessory protein) (V-ATPASE Ac45 subunit)		pdate)		470 AA	

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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and and characterization of hydrophobins-encoding cDNAs from the ectomycorrhizal basdiomycete Pisolithus tinctorius."; Gene 168:93-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYD-1
  SEQUENCE
                                                            PROSITE; PS00956; HYDROPHOBIN; Cell wall; Signal.
                                                                                                       SMART;
                                                                                                                                                               EMBL; U29605; AAC49307.1; -
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Tagu D., Nasse B., Martin F.;
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Boletales;
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                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: BELONGS TO THE FUNGAL HYDROPHOBIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=37468;
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                                                                                                                      PF01185; Hydrophobin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK026519; -; NOT_AN; HGNC:868; ATP6IP1.
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D16469; BAA03938.1; ALT_INIT.
AK026519; -; NOT_ANNOTATED_CDS.
                                                                                                     SM00075;
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                                                                                                                                             IPR001338; Hydrophobin.
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18.2%;
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N-S (IN REF. 3).
S -> F (IN REF. 3).
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      HYDROPHOBIN-1.
; 0A05E8D607DF4E33 CRC64;
                                             POTENTIAL
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RESULT 3
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ID Y65L,HORVU
ID Y65L,HORVU
ID Y65C,HORO
ID 15-DEC
DT 15-DEC
DT 16-OCT
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OS HOXIGEU
OC EURATY
OC SPERMIN
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Best Local Similarity
'hehes 2; Conserv
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Best Local
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01-FEB-1995
01-FEB-1995
15-DEC-1998
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of randomly selected cDNAs reveals the expression of stress-
and defence-related genes in the barley mutant albostrians.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Haisa; TISSUE=Leaf;
Hess W.R., Golz R., Boerner T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y65L_HORVU
048609;
SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                      precursor.
                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ222779; CAA10984.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                              YHR143W.
                                                                                                                                                                                                                                                                                                                           YHU3_YEAST
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(Rel.
1 33.4
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. 37, Last anno
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19865 MW;
                                                                                         Saccharomycetaceae;
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CHLOROPLAST (POTENTIAL).
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Pred. No. 4.9e
0; Mismatches
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. 5.6e-(
                                                                                         Saccharomyces.
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                                                                                                                                                                                                       intergenic region
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RESULT 5
OXYR_MA
AC P97926
DT OXYR_M
AC P97926
DT 15-JUL
DT 16-JUL
OX NCBLT
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and expression of the mouse oxytocin receptor gene.";
Mol. Cell. Endocrinol. 124:25-32(1996).
-!- FUNCTION: RECEPTOR FOR OXYTOCIN. THE ACTIVITY OF THIS RECEPTO
MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Kuteleostomi; Mammmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxytocin receptor (OT-R).
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15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
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           EMBL; D86599; BAA18995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kubota Y., Kimura T., Hashimoto K., Tokugawa Y., Nobunaga
Azuma C., Saji F., Murata Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97179034; PubMed=9027321;
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                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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36, Last sequence up
36, Last annotation
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Pred. No. 7.6e-07
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                            Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR OXYTOCIN. THE ACTIVITY OF THIS RECEPTOR MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-95116525; PubMed=7816817;
MEDLINE-95116525; PubMed=7816817;
MEDLINE-95116525; PubMed=7816817;
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                                                                                                                                                                                                    Rozen F., Russo C., Banville D., Zingg H.H.;
"Structure, characterization, and expression receptor gene.":
                                                                                                                                                                                                                                                                                                           Enkaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eurheria; Rodentia; Sciurognathi;
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                         REVISION TO 84.
                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 92:200-204(1995).
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                                                  CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Best Local
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                MEDLINE-97021444; PubMed-8867804; Yoshida K.-I., Fujinyra M., Yanai N., Fujita "Cloning and sequencing of a 23-kb region of genome between the iol and hut operons."; DNA Res. 2:295-301(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
DISULFID
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DOMAIN
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Bacteria; Firmicutes;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                              STRAIN=168
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-168 / BGSC1A1;
                                                                                                                                                                                                                                                                                                                                                                                                                       YXEK OR LP9C
                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative monooxygenase yxeK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P54950;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YXEK_B/.CSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1423;
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18.2%;
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Best Local
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Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwojlik S., Presecat E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schrobeter R., Scoffone F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.S. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones H., Holsappel S., Hosono S., Hullo M.F., Holsappel S., Hosono S., Hullo M., Holsappel S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z99124; CAB15988.1; -. SubtiList; BG11887; yxeK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
--- STMILARITY: BELONGS TO THE NTAA/SNAA/SOXA(DSZA) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T., Winters P., Wipat A., Yamanot H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-pc: Live bacterium Bacillo
                                            Bohne W., Ferguson D.J.P., Kohler K., Gross U.;
"Molecular characterisation of a developmentally expressed spore
protein from the human microsportidian Encephalitozoon cuniculi.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                    Submitted
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Encephalitozoon cuniculi.
Eukaryota; Microsporidia;
                                                                                                                                                                                                                                                                                                                                Spore wall
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30-MAY-2000
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30-MAY-2000
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                    -!- FUNCTION: SPORE WALL COMPONENT
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18.28;
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                                                                                                                                                                                                                                          Unikaryonidae;
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Pred. No. 8.9e-07;
0; Mismatches
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.; "Cloning of two mouse genes encoding alpha 2-adreneraic receptor subtypes and identification of a single amino acid in the mouse alpha 2-ClO homolog responsible for an interspecies variation in
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   ымы.; м97516;
                                                                                                 the European Bioinformatics Institute.
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                              Brochem.
                                                                                                                                                                                                                                          adrenoceptor subtype gene
                                                                                                                                                                                                                                                                      Chang Y.-H.,
                                                                                                                                                                                                                                                                                    MEDLINE-93250567; PubMed-8387367;
                                                                                                                                                                                                                                                                                                      STRAIN-DBA/2
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Mammalla; Eutheria; Rodentia;
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"Molecular characterization of a murine homologue of a murine shomologue of the conceptor subtype gene.";
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                                                                                                                                                                                                 chem. Mol. Biol. Int. 29:467-474(1993).
FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                       PROTEINS.
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    receptor (Alpha-2C adrenoceptor) (Subtype C4).

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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
MEDIINE-91244823; PubMed-1645350;
Lanier S.M., Downing S., Duzic R., Homey C.J.;
"Isolation of rat genomic clones encoding subtypes of
                                                                                                                              Voigt M.M., McCune S.K., Kanterman R.Y., "The rat alpha 2-C4 adrenergic receptor pharmacological subtype.";
                                                                                                                                                                                                                                                   MEDLINE-91126047; PubMed-1704126; Flordellis C.So., Handy D.E., Bresnahan M.R., Zannis V.I., G "Cloning and expression of a rat brain alpha 2B-adrenergic Proc. Natl. Acad. Sci. U.S.A. 88:1019-1023(1991).
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Alpha-2C adrenetyic receptor (Alpha-2C adreneeptor) (Subtype C4)
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Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                     Voigt M.M.,
                                                                                                                                                                                        MEDLINE-91130596; PubMed=1704314;
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                                                                                                          FMBS Lett. 278:45-50(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COA8HDF0302BF1FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; I
. 9.1e-07;
                                                                                                                                                 gene encodes a novel
                                                                                                                                                                       Felder C.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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    the alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Stewart A.,

Jagels K.,

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RESULT 11
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                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                    Matches
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DNA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                               PRINTS; PR00033; HTHASNC.
SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commencentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937425;
01-0CT-1994 (Rel. 30, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Transcription regulation; Activator; Complete proteome. INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stygene; SG10210; lrp.
InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC_FAMILY; 1.
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                DNA-binding; Transcription regulation; Activator. INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000485; ASNC_trans_reg. Pfam; PF01037; ASNC_trans_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U02276; AAA75466.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calvo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWIS: - PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucine-responsive regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRP_SERMA
                               \frac{\omega}{\omega}
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                                                                                                                               Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                             1 LSKRIGLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSKRIGLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LEP MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS. FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENES
                               LSKRVGLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSKRVGLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AA;
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87.5%;

    Mismatches

                                                                                                                                                      Score 35; DB 1; Length 163; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB Pred. No. 8.8;
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A -> G (IN REF. 1).
                                                                                                                                                                                                                               H-T-H MOTIF (POTENTIAL).
; 0940AC4C7937AE48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A0193595B8EBDE25 CRC64;
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBI, outstation
                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                               Gaps
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                                                                                                                               0;
                                                   RA Rutherford K., Ruther S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Stelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Garzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert R., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RT "Atture 415:871-880(2002)
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactokinase (EC 2.7.1.6) (Galactose kinase)
                                                                   PROSITE; PS00106; GALACTOKINASE; 1.

PROSITE; PS00627; GHMP_KINASES_ATP; 1.

Transferase; Kinase; Galactose metabolism; ATP-binding.

NP_BIND 157 167 ATP (POTENTIAL).
                                                                                                                                                                                                InterPro; IPR001459; mev_gal_kin.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00473; GALCTOKINASE.
PRINTS; PR00559; MEVGALKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Chrurcher C.M., Collins M., Connor R., Croolin A., Davis P., Feltwell T., Fraser A., Collins S., Coble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAL1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HDU2;
                                                                                                                                                                             TIGRFAMS; TIGRO0131; gal_kin; 1.
                                                                                                                                                                                                                                                                                                                                                         EMBL; AL512522; CAC21415.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                  InterPro; IPR000705; Galactokinase.
InterPro; IPR001745; GHMPknse_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CHMP KINASE FAMILY. GALK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21848401;    PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + D-galactose - ADP + D-galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Galactose metabolism; first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate.
                                                 519 AA;
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                                                   58385 MW;
     71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetaceae;
     Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetes;
                                                   5EE9C129896F8C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions on ong as its content is in no
  DB 1;
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Length 519;
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EMBL outstation

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                                             Matches
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16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
Hypothetical protein (
SPBC543.04.
                                                                                                                                                   Pfam; PF03666; UPF0171; 1.
                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHPO
                                                                                                                   Hypothetical SEQUENCE 5
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Churcher C.M., Collins M., Connor R., Gronin A., Davis P., Feltwell T., Fraser A., Collins S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hogson G., Honrsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
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                                           Similarity 6; Conserv
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                                                                                                                   585 AA; 66868 MW;
                                             Conservative
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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                                                            Score 35;
Pred. No.
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                                                                              DB 1; Length 585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region."; Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P21466; Q53282; Q45662;

01-MAY 1991 (Rel. 18, Created)

01-AGC-1991 (Rel. 19, Last sequence up

15-JUN-2002 (Rel. 41, Last annotation

305 ribosomal protein $4 (B$4).
                                                                                                                                                                                                                                                                                                                      Henkin T.M., Chambliss G.H., Grundy F.;
"Bacillus subtilis mutants with alterations in ribosomal protein S4.";
J. Bacteriol. 172:6380-6385(1990).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
-!- FUNCTION: PROTEIN S4 IS ALSO A TRANSLATIONAL REPRESSOR PROTEIN, IT
CONTROLS THE "TRANSLATION OF THE ALPHA-OPERON (WHICH CODUSE FOR S13,
S11, S4, RNA POLYMERASE ALPHA SUBUNIT, AND L17) BY BINDING TO 1TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grundy F.J., Henkin T.M.;
"The rpsD gene, encoding ribosomal regulated in Bacil us abbilis.";
J. Bacteriol. 173:4595-4602(1991).
     EMBL;
                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Higo K.I., Otaka M., Osawa S.; "purification and characterization of 30S ribosomal proteins from Bactilus subtilis: correlation to Escherichia coll 30S proteins."; Mol. Gen. Genet. 185:239-244(1982).
                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS4_BACSU
                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 S4 RNA-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein 84."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and analysis of the Bacillus subtilis rpsD gene, encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: |:|:||||
359 IANRLGISVSE 369
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$45404; AAB19387.1; -. 

%299119; CAB14944.1; -. 

M60889; AAA22716.1; -.
                                                       M59358; AAA22717.1; -. AF008220; AAC00397.1;
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RA Guiseppi G., Guy B.J., Hagda K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Perescan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
Ra Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sanlaın E., Schleich S., Schroeter R., Scoffone F.,
Saho T., Scanlaın E., Schleich S., Schroeter R., Scoffone F.,
Sak Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-96051385; PubMed=7584024; Ogasawara N., Nakai S., Yoshikawa H.; Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin."; DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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P37505;
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PROSITE; PS00632; RIBOSOMAL_S4; 1.
Ribosomal protein; rRNA-binding; Translation regulation; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
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HSSP; P81288; 1C05.
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60.0%;
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MISSING (IN MUTANIT RPSD2).
L -> LAGKL (IN MUTANT RPSD1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Winters P., Wipat A., Yamanoto H., Yamano K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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                                                                                                                                                                                                                                                                                                                                           Hypothetical protein SEQUENCE 201 AA;
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37 LSKKIGLTV 45
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non-profit institutions as long as its content
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2012 MW; 77A149C6F0979317 CRC64;
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Search completed: January 15, 2003, 11:21:33 Job time : 11.2857 sccs

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49
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## ALIGNMENTS

DR DR KW	22000E	RA RA RA RT	RA R	RESULT Q58439 AC Q AC Q DT 0 DT 0
InterPro; IPR00323; CorA. InterPro; IPR00323; CorA_transp. Pfan; PP01544; CorA; 1. TIGNEAMS; TIGN0383; corA; 1. Hypothetical protein; Magnesium; Cobalt; Transmembrane; Transport; Complete proteome.	Science 273:1058-1073(1996).  Science 273:1058-1073(1996).	Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fhirmmann J.L., Nguyen D., Utterback T.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk HP., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii".	McLhanococcus jannaschii.  McLhanococcus jannaschii.  Archaea: Euryarchaeota; Mcthanococci; Methanococcales;  Mcthanococcacca; Mcthanococcus.  McHl_TaxiD=2190;  [1]  [1]  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SETRAIN-JAL-1 / DSM 2561 / AFCC 43067;  STRAIN-JAL-1 / DSM 2561 / AFCC 43067;  MEDILINE-96337999; PubMod-8688087;  MEDILINE-96337999; PubMod-8688087;  Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Reich C.I.,  Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  Kerlavage A.R., Dougherty B.A., Tomb JF., Adams M.D., Reich C.I.,	OUT 1 439 Q58439 PRELIMINARY; PRT; 317 AA. Q58439; O1-AN-1998 (TrEMBLTel. 05, Created) O1-JAN-1998 (TrEMBLTel. 05, Last sequence update) O1-JUN-2002 (TrEMBLTel. 21, Last annotation update) Putative magnesium and cobalt transport protein CORA.

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RESULT
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
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STRAIN-AV19 / DSM 6324 / JCM 9639;
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Archaea; Euryarchaeota;
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 Mismatches

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RESULT 4
Q982L8
ID Q982L8
Q982L8
Q982
AC Q982
DT 01-C
DT 01-N
DD HYPK
GN MILP
OS Rhi
OG Bac
OC Bac
OC Phy
OX NCE
RN [1]
RP SE(
RV ME)
RX ME
RA Ka
RA K
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ID Q
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Best Local S
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Best Local S
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                                                                 Q9Z4G7
Q9Z4G7;
           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
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01-0CT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochicuki Y., Nakayama S., Nakazaki N., Slimpo S., Suqimoto M., Talenchi V., Nakayama S., Nakazaki N., Slimpo S., Suqimoto M.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00893; DUF7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 7:331-338(2000).
EMBL: AP003015; BAH54438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium lott.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
McMurray A.A.;
McMurray A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000390; DUF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takauchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                      G
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01-027-2001 (TrEMBLrel, 18, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last annotation updat
Hypothetical protein ml19408.
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Pfam; PF01
                                                                                                                                                                                                                                           1 LSKRIGLSV 9
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EMBL; Z83218; CAB05691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for investigating biology ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613;
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                                                                                                                                                                                                   LSKRIGLSL 105
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1; PF01461; 7tm_4; 1.
ENCE 352 AA; 40920 ...
                                                                                                                                                                                                                                                                                          Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome, 117 AA; 12444 MW; 1D01801CDB574AF3 CRC64;
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Similarity 63.6%;
7; Conservat:
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                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                      75.5%;
88.9%;
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Last sequence update)

    Mismatches

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                                                                                                                                                                                                                                                                                                                           Score 37;
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                                                                                                                                                                                                                                                                     Gaps
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RESULT
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Best Local S
Matches 6
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Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArcllano K., Johnson R., Linton L., McGwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                       Methanosarcina acetivorans.
Archaea: Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
                                                                  STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-S.typhimurium; PLASMID-INCN R46; Belogurov A.A., Hall R.M., Winans S.C., Woodgate R.; "Complete sequence of R46 and its deletion derivative, I Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; U72482; AAD17386.1; -.
                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                             Predicted protein
                                                                                                                                                                                                                                       01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Belogurov A.A., Delver E.P., Rodzevich O.V.; "Plasmid pKM101 encodes two nonhomologous antirestriction proteins (ArdA and ArdB) whose expression is controlled by homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel.
Hypothetical 8.5 kDa pro
                                                                                                                        NCBI_TaxID=2214;
                                                                                                                                                                                 MA2554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Plasmid.
SEQUENCE 79 AA; 8482 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium; PLASMID=I
MEDLINE=93328690; PubMed=8393008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Organization of the leading region of IncN plaregulation controlled by COP sequence elements
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                                                                                                                                                                                                                                                                                                                                      LAKKLGITVSE 79
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a; Proteobacteria; gamma subdivision;
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6 Conser
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                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                      73.5%;
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Pred. No. 13;
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Q8XXI6
ID Q8
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Best Local
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol, 183:4823-4838
EMBL; AE007644; AAK79294.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
WEDLINE-21359325; PubMed=1146286;
Noelling J., Breton G., Omelchenko, M.V., Makarova K.S., Zeng Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001
01-DEC-2001
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   Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; beta subdivision; Ralst
                                                                            DALR OR RSC2127 OR RS01506
                                                                                                                   protein.
                                                                                                                                      Putative transcriptional regulator (Repressor) transcription regulator
                                                                                                                                                                                                                                                                                                                       91XX80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPk003740; DUF161.
Piam; PF02588; DUF161; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterium Clostridium acetobutylicum.", J. Bacteriol, 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAC1325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q97.JG0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1488,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSKRIGLSVSE
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteome.
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1 (Trembirel 18, 1
1 (Trembirel 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12:532-542(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30797 MW;
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54.5%;
                                                                                                                                                                          20, Created)
20, Last sequence update)
20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9, Last annotation update)
protein, YitT (B.subtilis) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36;
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51A2742392A0CB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0A84089E7430MD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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43;
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                                                                                                                                                                          update)
Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeng
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RESULT 10
Q9I0X3
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Q93SR2
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Best Local
                                                                                                                                                                                                            Query Match
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 01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative muconate cyclofsomerase I CatB.
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                                           Q9I0X3
                                                        Q910X3
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                             PROSITE; PS00908; MR_MLE_1; UNKNOWN_1.
PROSITE; PS00909; MR_MLE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                        Pfam; PF01188; MR_MLE; 1. Pfam; PF02746; MR_MLE_N; 1.
                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2001) to the EMBL; AY026914; AAK52296.1;
                                                                                                                                                                                                                                                                                                                                                              originated from the strain
                                                                                                                                                                                                                                                                                                                                                                          Pieper D.H.; "Cloning, is
                                                                                                                                                                                                                                                                                                                                                                                                  Totevova S., Armengaud J., Cajthaml T., Demnerova K., Brenner V.,
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-P111;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q93SR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
EMBL; AL646068; CAD15834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia
                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=305;
                                                                                                                           118 KRLGLAVSE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 LSKRYGLSMCE 80
                                                                                                                                                                                Local Similarity les 7; Conser
                                                                                                                                                     3 KRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LS RICESVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                   IPR001354; MR_MLE.
                                                                                                                                                                                                                                                                                                                                                                          isolation and expression of benzoate 1,2-dioxygenase
                                                                                                                                                                                                                                     373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 AA; 33903 MW;
(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
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                                                       PRELIMINARY;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                     40131 MW;
                                                                                                                                                                                            73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                              Pseudomonas putida P111
 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                            Score 36; DB
Pred. No. 68;
                                                        PRT;
                                                                                                                                                                                                                                     E7E791D73B8CC6F4 CRC64;
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                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 AA.
                                                          373 AA.
                                                                                                                                                                                                         DB 2; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 315;
                                                                                                                                                                                0;
                                                                                                                                                                                Indels
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           RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., None H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysahi Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-EMBRYONIC LIVER; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TERMBLEEL. 17, Created)
01-JUN-2001 (TERMBLEEL. 17, Last sequence update)
01-JUN-2002 (TERMBLEEL. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9CS06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01188; MR_MLP; 1.

Pfam; PF02746; MR_MLE_N; 1.

PROSITE; PS00908; MR_MLE_1; 1.

PROSITE; PS00909; MR_MLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muconate cycloisomerase I.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaperonin subunit 8 (Theta) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CS06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004678; AAG05897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATS OR PA2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01354; MR_MLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 KRLGLAVSE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. 373 AA; 40045 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMUC
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77.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949BB0FAB3744E76 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Hayashizaki Y.;

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RESULT 13
Q8U425
ID Q8U42
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Best Local :
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Best Local
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  Q8U425
                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               Q9WVS5; PRELIMINARY; PRT; 547 AA.
Q9WVS5;
01-WOV-1999 (TrEMBLrel. 12, Created)
01-WOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Chaperonin containing TCP-1 theta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS:00751; TCP1_2; 1.
PROSITE; PS:00995; TCP1_3; 1.
ATP-binding; Chaperone.
NON_TER 458 458
                                                                                                                              PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
ATP-binding; Chaperone.
SEQUENCE 547 AA; 59568 MW;
                                                                                                                                                                                                                                                 Kubota H., Yokota S., Yanagi H., Yura T. "Structures and co-regulated expression cytosolic chaperonia CCT subunits."; Eur. J. Biochem. 262:492-500(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                             InterPro: IPR002194; Chaperonin_TCP-1.
InterPro: IPR002423; Cpn60/TCP-1.
Pfam; PP00118; Cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                        CCT8 OR CCTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
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InterPro; IPR001844; Chaprnin_Cpn60.
InterPro; IPR001834; Chapynin_Cpn60.
InterPro; IPR004233; Cpn60_TCP-1.
Pfam; PF00118; cpn60_TCP1; 1.
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HSSP; P48424; 1A6D.
MGD; MGI:107183; Cct8.
                                                                                                                                                                                                                      MGD; MGI:107183; Cct8.
                                                                                                                                                                                                                                         EMBL; AB022161; BAA81879.1;
                                                                                                                                                                                                                                                                                          MEDLINE=99269022; PubMed=10336634;
                                                                                                                                                                                                                                                                                                  STRAIN=129SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                   120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 RIGLSVSE 114
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                                                                     RIGLSVSE 11
                                                                                                                                                                                                                               P48424; 1A6D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conserv
                                                                                                 Similarity
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                                                                                        73.5%; Score 36; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  PRELIMINARY;
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                                                                                                                              59568 MW;
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Pred. No.
   PRT;
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                                                                                                                               6BC34987F74B94CE CRC64;
                                                                                         Mismatches
   914 AA
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                                                                                                 DB 11; Length 547; 
1e+02;
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RESULT 15
Q9AHY8
ID Q9AHY
AC Q9AHY
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE LTP (
GN LRP.
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086256
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Best Local
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Best Local
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         Lrp (Fragment).
                                                          Q9AHY8
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=571;
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                                                                                                                                                                                                                                                                                                                      Klebsiella
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                                                                                                          34 LSKRVGLS
                                                                                                                            1 LSKRIGLS
                                                                                                                                                                                                                                                 REGULATORS
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086256;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Leucine responsive element (Fragment).
Q9AHY8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               Albrecht C., Kleiner D.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus Submitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL; AE010151; AAL80394.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus furiosus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alanyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8U425;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aminoacyl-tRNA synthetase; Complete proteome. SEQUENCE 914 AA; 104906 MW; 467F593731BD8BC1
                                                                                                                                                                                                                                                                                                                      DNA-binding; Transcription regulation. NON_TER 51 51
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000485; ASNC_trans_reg;
PRINTS; PR00033; HTHASNC.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y16963; CAA76565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella oxytoca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 VAKRYGISVEE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                7; Conserv
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                                                                                                                                                                                                                                Conservative
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                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                              41
                                                                                                                                                                                                                                                                                                     5857 MW;
                                                                                                                                                                                                                                               71.4%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                             Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.8e
4; Mismatches
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                                                                        PRT;
                                                                                                                                                                                                                              Mismatches
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No.
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                                                                       72
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1.8e+02;
                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                               Length 51;
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Search completed: January 15, 2003, 12:36:03 Job time: 32.5714 secs
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OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Photorhabdus.

OX NCBI_TaxID=29488;

RN [1]

RN SEQUENCE FROM N.A.

STRAIN=NC19;

RX GIBAIN=NC19;

RX MEDLINE=2122553; PubMed=11325940;

RX MEDLINE=2122553; PubMed=11325940;

RX MEDLINE=2122553; PubMed=11325940;

RY MEDLINE=212253; PubMed=11325940;

RY MEDLINE=2122553; PubMed=1132594
                                                                                                                                                                                                                                                                                               Query Match 71.4%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORS
EMBL; AF288086; AAK16099.1; -.
InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
PRINTS; PR00033; HTHASNC.
SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00519; HTH_ASNC, FAMILY; 1.
DNA-Dinding; Transcription regulation.
NON_TER 72
SEQUENCE 72 AA; 8407 MW; 803932BD88EI
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34 LSKRYGLS 41
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Minimum DB
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SIDS2/gcgdata/geneseg/genesegp-embl/AA199.DAT:

SIDS2/gcgdata/geneseg/genesegp-embl/AA200.DAT:

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Arabidopsis thalia
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## ALIGNMENTS

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Arabidopsis thaliana. 2000EP-0301439 990S-0125788. 990S-0126264. 990S-0126785. 990S-0127462. 990S-0128234. 990S-0128714. 990S-012874. 990S-0129845. 99US-0123180 99US-0123548 99US-0121825

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RESULT 2
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ID AAG4541
AC AAG4
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 99US-0125788.
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99US-0127462.
99US-0127462.
99US-0128734.
99US-0128945.
99US-0130477.
99US-013049.
99US-013049.
99US-0131449.
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99US-0136782
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99US-0137702
99US-0137702
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99US-0137840
99US-0139452
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99US-0132863.
99US-0134256.
99US-0145085
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US-0145913. US-0145919. US-0145919. US-0145919. US-0145919. US-0145919. US-0145919. US-0145919. US-0145919. US-0147303. US-0147303. US-0147103. US-0150566. US-0150566. US-0150566. US-0150566. US-0150566. US-0150566. US-0150566. US-0150566. US-0150770. US-0150777. US-0150777. US-0150777. US-0150777. US-0150777. US-0160771. US-0160771. US-0160771. US-0160771. US-0160771. US-0160771. US-0160770. US-0160770. US-0160770. US-0160814. US-0160980.		1 \$\rightarrow \text{Q}	
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 25-FEB 1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
01-APR 1999
06-APR 1999
06-APR 1999
16-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
21-MAY 1999
14-MAY 1999
18-MAY 1999
21-MAY 1999
21-MAY 1999
21-MAY 1999
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25-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
29-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG49540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana protein fragment SEQ ID NO: 62683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0161405.
99US-0161359.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0161993.
   9905-0121825.
9905-0125788.
9905-0125788.
9905-0125788.
9905-0127462.
9905-0127462.
9905-012845.
9905-013077.
9905-0130449.
9905-0130649.
9905-013048.
9905-0132485.
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Pred. No. 2.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; _____

5. 2.3e+02;

5. 2.3e 9;
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     14-JUN-1999
116-JUN-1999
116-JUN-1999
117-JUN-1999
118-JUN-1999
119-JUN-1999
119-JU
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27-MAY 1999;
28-MAY 1999;
01-JUN 1999;
03-JUN 1999;
04-JUN 1999;
07-JUN 1999;
08-JUN 1999;
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|-1999;
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990S-0139453.
990S-0139453.
990S-0139456.
990S-0139456.
990S-0139461.
990S-0139461.
990S-0139462.
990S-013962.
990S-013962.
990S-013962.
990S-01408917.
990S-0140823.
990S-0140823.
990S-0140823.
990S-0141287.
990S-0142803.
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990S-0142803.
990S-0142803.
990S-0143642.
990S-0144005.
990S-0144005.
990S-0144225.
990S-0144331.
990S-0144333.
990S-0144333.
990S-0144352.
990S-0144352.
990S-0144814.
990S-014508.
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99US-0136392
99US-0136782
99US-0137222
99US-0137528
99US-0137502
99US-0137724
99US-0138047
99US-0138647
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0;

Gaps

0;

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9908-0147038
9908-0147302
9908-0147302
9908-0147303
9908-0147303
9908-01477303
9908-01477416
9908-0147416
9908-0148171
9908-0148171
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9908-0149422
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9908-0161361
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AAG49539
  Дb
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PR
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Best Local Similarity 18.2%;
Matches 2; Conservative
25-MAR 1999
29-MAR 1999
01-APR 1999
06-APR 1999
16-APR 1999
16-APR 1999
19-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
30-APR 1999
30-APR 1999
14-MAY 1999
06-MAY 1999
06-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG49539
                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSSSSSSSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     2000EP-0301439
9908-0132407
9908-0132486
9908-0132486
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9908-0132486
9908-013427
9908-013427
9908-013427
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9908-0135353
9908-0135629
9908-0136221
9908-0137222
9908-0137222
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99US-0130449.
99US-0130510.
99US-0130891.
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99US-0126785
99US-0127462
99US-0128234
99US-0128714
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99US-0123548.
99US-0125788.
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99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9; DB 21;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 62682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9,
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03-AUG-1999
04-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
06-AUG-1999
110-AUG-1999
111-AUG-1999
113-AUG-1999
113-AUG-1999
113-AUG-1999
12-AUG-1999
13-AUG-1999
13-SEP-1999
14-SEP-1999
15-SEP-1999
17-AUG-1999
17-AUG-1999
18-AUG-1999
18-AUG-1999
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                                                           AAB58817;
                                                                                               AAB58817 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                                                                                                    allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoi
                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacteria; antifungal; antiparasitic and cardiant activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAF58711 - AAF59128. The DNA and protein sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular
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                                                                                                                                                Sequence
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nassay, genetic mapping, gene expression control, promoter; sequence.  thaliama.  2000EP-0301439  99US-0121825  99US-0121826  99US-0121826  99US-0127788  99US-0126234  99US-0126234  99US-0126234  99US-0126234  99US-0126234  99US-013624  99US-01362  99US-0	Arabidopsis thaliana protein fragment SEQ ID NO: 1803. Protein identification; signal transduction pathway; metabolic pathway;
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           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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;-0154039.
                                                                                                                376
                                                                                                                                                                                                     Score 9; DB 2
Pred. No. 2.9e
0; Mismatches
                                                                                                                                                                                                      0;
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  29-MAR 1999
01-APR 1999
06-APR 1999
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18-JUN-1999
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01-JUN-1999;
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21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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30-APR 1999
04-MAY 1999
05-MAY 1999
06-MAY 1999
06-MAY 1999
07-MAY 1999
11-MAY 1999
14-MAY 1999
14-MAY 1999
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23-MAR-1999;
25-MAR-1999;
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18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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05-MAR-1999;
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18-JUN-1999;
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19-MAY-
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07-JUN-1999;
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14-MAY-
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18-JUN-1999;
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        9908-013632

9908-0137528

9908-0137522

9908-0137502

9908-0137502

9908-0138094

9908-013847

9908-013845

9908-013945

9908-013945

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99US-0134256
99US-0134218
99US-0134219
99US-0134271
99US-0134776
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99US-0134971
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99US-0132407.
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99US-0128234.
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99US-0123180.
99US-0123548.
99US-0125788.
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8006
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  99US-0140991
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99US-0126785
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S-0131449.
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-0136021
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02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 09-JUL-1999;

30-JUN-1999; 01-JUL-1999; 01-JUL-1999;

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RESULT 10
AAY21800
ID AY21
XX
AC AAY21
XX
DE Human
XX
Vacuc
KW Vacuc
KW Vacuc
KW Cance
XX
Homo
XX
10593
XX
PD 03-AL
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PF 28-OC
XX
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Best I
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16-SEP 1999
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28-SEP 1999
29-CT 1999
04-OCT 1999
07-OCT 1999
13-OCT 1999
13-OCT 1999
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23-OCT 1999
24-OCT 1999
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28-OCT 1999
29-OCT 1999
                   28-OCT-1997;
                                                            03-AUG-1999
                                                                                                    US5932444-A
                                                                                                                                                                                  cancer; immune disorder; human.
                                                                                                                                                                                                 Vacuolar ATPase subunit AC45; HAC45; vacuolar ATPase; ion transport;
                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                        20-SEP-1999
                                                                                                                                                                                                                                                                                                                                  AAY21800;
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                                                                                                                                                                                                                                             vacuolar ATPase subunit AC45 (HAC45).
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2; Conservative
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990S-0154019
990S-0155486
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990S-0155486
990S-015785
990S-015829
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990S-0160814
990S-0161804
990S-0161903
990S-0161903
                   97US-0959011.
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                                                                                                                                                                                                                                                                                                                                                                       470
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Pred. No. 2.9e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                       AA
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99US-0141287 99US-0141287 99US-0142055 99US-014205 99US-014203 99US-014203 99US-014203 99US-0144203 99US-014406 99US-014408 99US-014408 99US-014433 99US-014521 99US-015106 99US-0151080 99US-015363 99US-015363

20-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 27-JUL-1999 28-JUL-1999 29-JUL-1999 21-JUL-1999 21-JU

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RESULT 11
AAM93671
ID AAM93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a human vacuolar ATPase subunit AC45 (HAC45). Vacuolar ATPase provides most of the energy required for ion transport processes within the vacuolar system in eukaryotic cells. The polypeptide can be produced recombinantly by culturing host cells transformed with a vector comprising the HAC45 nucleic acid. Compositions comprising the HAC45 polynucleotide sequences are useful in the treatment of cancers and immune disorders. The sequence complementary to the HAC45-encoding sequence is useful for inhibiting expression of naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-F; 32pp; English
The invention relates to primers for synthesising full length CDNA
                         Claim 8; SEQ ID NO 3556; 1380pp + sequence listing; English.
                                                830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                     N-PSDB; AAK94606.
                                                                                                                        Wakamatsu A,
                                                                                                                                                                                                                                          07-JUL-2000; 2000EP-0114089.
                                                                                                                                                                                                                                                                                             EP1130094-A2
                                                                                                                                                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide, SEQ ID NO: 3556.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM93671 standard; Protein; 470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1997;
                                                                                                    WPI; 2001-524255/58.
                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                         02-MAY-2000;
                                                                                                                                                                                                              08-JUL-1999;
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       AAM93671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vacuolar ATPase subunit AC45 for treating cancer and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-443597/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                     11-JAN-2000;
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                                                                                                                                       Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                      2000JP-0118774.
2000JP-0183765.
                                                                                                                        Sugiyama T,
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                                                                                                                                                                                                               99JP-0194486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
18.2%;
                                                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shah P;
                                                                                                                           Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                      Hayashi K,
                                                                                                                           Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
. 3.2e+02;
                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 470;
                                                                                                                           Otsuki T,
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                                                                                                                                      Kawai Y;
                                                                                                                           Koga H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA casily without any special methods. The present sequence is a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO
                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for clucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 24441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24441; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical.
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                                                                                (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                           interactions
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es 2; Conserv
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                                                                                                                                                                                                                                                                                                                                            ABL09986
803 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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18.2%;
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Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
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                                                                                                                                                                                    The invention is
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Sequence

Query Match

Length 803;

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Matches 2; Conserv
                                                                2558 LSSSTTTSTTE 2568
                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling
ABB68812 standard; Protein; 99 AA.
                                                                                                                                                                              Sequence
                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL38511), expressed DNA
                                                                                                                                                                                                                                                                                                        cell-cell
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 31983; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                       specification,
                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                        interactions
                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL12500
                                                                                                                                                                                                                                                                                                        interactions in higher eukaryoles for the development of
                                                                                                                                                                                                                                                             (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                               2768 AA;
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
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18.2%;
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Pred. No. 4.1e+02;
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7e+02;
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30-APR-2001 AAB79413;

(first entry)

AAB79413 standard; Protein; 104 AA.

SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;

Corynebacterium glutamicum; carbon metabolism and energy production;

Corynebacterium glutamicum SMP protein sequence SEQ ID NO:342.

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RESULT 15
AAB79413
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                                                                                                                                                                                                                                                                                                        insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                           useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 33228; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more
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cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (II) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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14-JUL-1999;
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09-JUL-1999
09-JUL-1999
                                                                                                                                                                                                                  AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Page 622-624; 1246pp; English.
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                                    Score 8;
Pred. No.
                             Mismatches
                                    DB 22; Length 104; 1e+03;
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Search completed: January 15, 2003, 11:20:12 Job time: 32.2857 secs

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Listing first 45 summaries
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US-08-959-011-1
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; TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS;FOR ENHANCED CYTOTALICITY AND IMAGING
; NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;SEQ ID NO:42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/
FILING DAPE: 07-AUG-1989
PRIOR APPLICATION NUMBER: 232,337
FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                                  APPLICANT: Hillman, Je
APPLICANT: Shah, Purvi
APPLICANT: Corley, Nei
                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VACUOLAR ATPASE SUBUNIT AC45
                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                           COUNTRY:
                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                       13 LANANANASE 23
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US-09-562-737-79
US-08-482-847-20
US-08-482-847-24
US-09-247-738-24
US-09-247-738-24
US-09-296-715-24
US-09-296-715-24
US-09-296-715-4
US-08-705-875A-4
US-09-125-891-2
US-09-125-891-2
US-09-125-891-2
US-09-125-891-2
US-09-231-27-2
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US-09-231-27-2
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Pred. No. 4.6;
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Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 21, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 79,
Sequence 20,
Sequence 20,
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US-09-128-155-11
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Best Local Similarity 10.2
Conservative
                                                                                                                                                                                                                                        SOFTWARE: Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 243, Application US/09199637A Patent No. 6355411
                                                                                                                     Matches
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/199,637A CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,517
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TITLE OF INVENTION: SEQUENCES AND USES THEREOF FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                          GENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                            123 LISSAASTTTE 133
                                                                                                                    Local Similarity
nes 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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Mahajan-Miklos, Shalina
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18.2%;
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18.28;
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                                                                                                                                  Score 8; DB 4; Length 134; Pred. No. 88;
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Pred. No.
                                                                                                                     Mismatches
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Query Match
Best Local Similarity
Taiches 2; Conserva
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US-09-128-155-7
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                                                                                                     ; GENERAL INFORMATION: ; APPLICANT: Pan, Yan;
                                                                                                                                           ; Sequence 2, Application US/09128155 ; Patent No. 6117654
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Patent No. 6117654
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                                      TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
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EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001 CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
                    CURRENT APPLICATION NUMBER: US/09/128,155
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les 2; Conservative
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18.28;
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18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 8; DB 3; Length 167; Pred. No. 97;
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Pred. No.
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89;
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US-09-293-625-2
                                                                                                                                                                                                                                                                                                                                                                                                          US-08-245-295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/293,625
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 2 - *
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08245295
Patent No. 5700658
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Matches 2; Conservative
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APPLICANT: MCDOnnell, Peter C
TITLE OF INVENTION: INVERTLEUKIN-1 HOMOLOGUE, IL-1H4
FILE REFERENCE: GP-70607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                             APPLICANT: Gallatin, W. Michael APPLICANT: Kilgannon, Patrick D. TITLE OF INVENTION: ICAM-4 Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 178
                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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Local imilarity 18.2%;
nes 2; Conservative
 APPLICATION NUMBER: US/08/245,295 FILING DATE:
                                                                                                                                                                                                   STREET: 233 Sc
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 LASSISSASAE 104
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                                                                                                                                                                COUNTRY:
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Pred. No. 1.1e+C
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Pred. No. 1e+02;
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PRIOR APPLICATION DATA:
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                   FILING DATE:
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Query Match
Best Local Similarity
watches 2; Conserve
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           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
'FILING DATE: 27-JAN-1S:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
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TELECOMMUNICATION INFORMATION: 312-474-6300
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APPLICATION NUMBER:
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TELEFAX: 25-3856
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                                                                                                                              APPLICATION NUMBER: FILING DATE:
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TYPE: amino acid
                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                STREET: 233 Sc
CITY: Chicago
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REGISTRATION NUMBER: 2:
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05-AUC-1993
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                                                                     US 07/827,689
               US 07/889,724
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Pred. No. 2.1e+02;
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                                PRIOR APPLICATION DATA:
                                                                                     FILING DATE: 26-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                       APPLICATION NUMBER: US 0: FILING DATE: 27-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,984A
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                                                  APPLICATION NUMBER: US 07/894,061 FILING DATE: 05-JUN-1992
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FILING DATE:
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VENTION: ICAM-4 Materials and Methods
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22-JAN-1993
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Best Local 9
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                                PRIOR APPLICATION DATA:
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                                                                                  FILING DATE: 26-MAY-1992 PRIOR APPLICATION DATA:
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TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
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ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/102,852
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 FILING DATE:
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                     APPLICATION NUMBER:
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                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                  APPLICATION NUMBER:
                                                                                                                                                                     APPLICATION NUMBER: US 07/827,689
                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                  60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                               Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-3856
                                                                                                                                                                                                                                                                                                                                                                                               Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                               233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312-474-0448
                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WP, W. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                        TBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshall, O'Toole, Gerstein, Murray & Borun
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22-JAN-1993
                                                                                                                                                     27-JAN-1992
                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.4%;
18.2%;
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                                                                                                                     US 07/889,724
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                  US 08/009,266
                                                                  US 07/894,061
                                                                                                                                                                                                                                          US/08/485,604
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Pred. No. 2.1e+02
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 08/102,852

Gaps

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; MOLECULE TYPE: protein US-08-485-604-2
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                                                       FILING DATE: 05-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DAYA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICAMT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEGUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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     FILING DATE: 18-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 LVATATATASE 292
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0' FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                        APPLICATION NUMBER:
                                                                                             APPLICATION NUMBER:
                                                                                                                               FILING DATE:
                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/487,595
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
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Local Similarity 18.28;
es 2; Conservative
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REFERENCE/DOCKET NUMBER: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917 amino acids
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                                                                                                                               22-JAN-1993
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                                                                                                                                                                                                    US 07/894,061
                                        US 08/245,295
                                                                                           US 08/102,852
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Pred. No.
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. 2.1e+02;
:ches 9; Indels
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US-08-180-524-1
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SEQ ID NO 4463
LENGTH: 2137
                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tripp,
APPLICANT: Lusk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                     APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               1701 LSDSTSTSTSE 1711
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LENGTH: 917 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS
                          APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                     APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
                                                                                                                                               APPLICANT:
                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELLEFAX: J. 25-3856
                     NUMBER OF SEQUENCES:
                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILLIAMS, JR. JOSEPH A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                   1 LXXXXXXXXX []
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Similarity 18.28;
2; Conservation
                                                                                                                                                                                                                                                      , Application US/08180524 5849537
                                                                                                                                                          Huige, Nick
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                                                                                                                                                                               Rhodes,
                                                                                                                                                                                                Lusk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                         Edward
                                                                                                                                                                                                                     Matthew
                                                                                                                                                                               Thomas
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18.28;
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0; Mismatches
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Pred. No.
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0. 2.1e+02;
9;
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. 3e+02;
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Search completed: January 16, 2003, 11:04:51 Job time : 1662.14 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                 Score
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3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp·emb1/AA1999.DAT:*
/SIDS2/gcgdata/geneseq/genescqp·emb1/AA2000.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embi/AA2002.bAF:*
                                                                                                                                                                                                                                                                                                                              Length DB
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690
754
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AAR23171
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AAM48268
AAR23174
AAR23173
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Native DNA polymer
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	יי ב	256	256	182	119	119	91	37	1046	956	889	822	549	165	79	62	59	779	532	532	502	502	502	408	382	382	373	79	1043	90	584	555	548	548	258
t	S	20	20	20	23	22	23	22	20	22	23	23	23	38	20	18	23	21	21	21	23	21	21	20	21	21	23	20	22	19	22	22	20	16	21
1112000	AAH08750	AAY38896	AAY38895	AAY38894	ABB49471	AAE11177	ABP05858	AA007530	AAY29106	AAB93299	AAE20268	AAU79551	Ани29511	AAW20621	AAY07970	AAW20505	ABP06956	AAY94997	AAG43428	AAG23937	АВН91449	AAG43429	AAG23938	AAY60505	AAG43430	AAG23939	AAH23653	AAY12988	ABG08827	AAY85848	ABG21966	96	AAY07062	58	AAB43412
naman metanocoretn	ST BO DESCRIPTION	SSATIA	isseria	യ		Bacillus anthracis		polyp	acid sec	protein seq	man lung spe	S. salivarius 1,6-	reptococcus		an '		ORFX pro	pr+	Arabidopsis thalia		V	~	opsis t	سو		tha	lising and	secre	el human d	ieumoni.	l human	l human diagn	l cancer asso	CCT-theta s	Human cancer assoc

## ALIGNMENTS

RESULT 1

AAB47796 standard; peptide;

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AAB4
XX
DE
NAIL
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XX
V
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                                                                                                                                         WPI; 2002-076891/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Native DNA polymerase motif #6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000US-198336P.
                                                                                                                                                                                                                                          n CM, Gelfand DH,
Wang AM;
                                                                                                                                                                                                                                                                                  Higuchi RG,
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Reverse transcribing an  $\mathtt{RNA},$  comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture

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RESULT 2
AAM48268
ID AAM4
XX AAM4826
AC AAM4
XX DN AAM4
XX DN AAM4
XX UNA
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAB47791-97 represent the native forms of motifs derived from NA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine
                                                                                                                                                                                                                                                                                        Reverse transcribing an RNA, comprises performing a revertranscriptase polymerase chain reaction amplification of using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2000; 2000US-198336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; reverse transcription; primer; divalent cation; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM48268 standard; Peptide; ll AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family dyes. The method of the invention is useful in reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                                                                                                                                           Page 7; 23pp; English.
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Pred. No. 0.0014;
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Higuchi
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                                                                                                                                                                                                                                                                                                                                                         a reverse
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Best Local
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                                                                                                                                                                                                                                                                                                                                             28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                              activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and high temp. DNA sequencing the absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined may facilitate higher sensitivity allelic discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA polymerase's ability to incorporate dideoxynucleotides labelled in fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                      The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-ILE 284 Taf. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                               Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for
                                                                                                                                                       Claim 11; Page 59;
                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermosipho
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                                                                                                                                                                                 in e.g. PCR, sequencing and detection assays
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                                                                                                                                                       185pp; English.
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                                                                                                                                                                                                                                                                                        DH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplification; SSR; sequencing; PLCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with
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polymerase ligase chain reaction (PLCR) assay. An enhanced amt..of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target

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AAR23173
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                        amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular
                                                                                                                                                        The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-THR 204 Taf. having a different amt. of 5'.3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinations having 5'-3' exonuclease activity to a complete lack of
proteins having 5'-3' activity.
                                                                                                                                                                                                                      Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant thermostable DNA polymerase enzyme MET-THR 204 TAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR23173 standard; Protein; 690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
            regions of the enzymes can be used to prepare a range of recombi proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                  are useful
                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ24333
                                                                                                                                                                                                                                                                                                                                                          Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR23173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity.
                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 LSKRICLSVSE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                              1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      609 AA;
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                                                                                                                                                                                                                                                                                                                                                        Gelfand
                                                                                                                                                many recombinant DNA techniques, esp. nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                90US-0590213.
90US-0590466.
90US-0590490.
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1..2 . . *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                               recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant
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RESULT 5
AAR23172
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Best Local S
Matches 11
                                                                                                    present in the given sequence at position 140 is an Asp.

Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR. self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5.3 nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5.3 exonuclease activity may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
28-SEP-1990;
                                   desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                               mutant designated MET-GLU 140 Taf. having a different amt. of 5' exonuclease activity than the native enzyme. However the residue
                                                                                                                                                                                                               The sequence is that of a mutant of Thermosipho africanus polymerase
                                                                                                                                                                                                                                                       Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5: 3: exo nuclease activity - having conserved regions mutated or deleted, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR23172 standard; Protein; 754 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                        See also
                                                                                                                                                                                                                                                                                in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ24332
                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                 Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermosipho airicanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant thermostable DNA polymerase enzyme MET-GLU 140 TAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR23172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAR23140-79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                         (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                        AAR23140-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                690 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Gelfand
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90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "residues 2-139 deleted
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                        and
                                                                                                                                                                                                                                                                                                                                                                                 DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence"
                        AAR23722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 1
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the native
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                amplification by PCR, self-sustained sequence replication (SSR) and high temp. NNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced aut. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant MET-TYR 94 Taf. having a different amt. of 5'-3' exonuc. activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-TYR 94 Taf. having a different amt. of 5'-3' exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nucl activity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant thermostable DNA polymerase enzyme MET-TYR 94 TAF
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                                                                                                                                                                 See also AAR23140-79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CETU ) CETUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermosipho africanus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1992-150885/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP.
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90US-0590466.
90US-0590490.
                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "residues 2-93 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No. 0.15;
Mismatches
                             Score 49; DB 1
Pred. No. 0.16;
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                                                       DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                esp. nucleic acid
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                                                    Length 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

В Qy

704 LSKRIGLSVSE 714

1 LSKRIGLSVSE 11

Query Match Best Local Matches

Similarity

100.0%; Score 49; DB 1 llarity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches

DB 13; Length 856;

0

0, Gaps

0;

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RESULT 7
AAR23170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
 28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                           activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCk, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced aut. of
                                          5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinar proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                           WP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR23170 standard; Protein; 856 AA
Sequence
                                                                                                                                                                                                                     The sequence is that of a mutant of Thermosipho africanus polymerase mutant MET-LEU 38 Taf. having a different amt. of 5'-3' exonuclease
                                                                                                                                                                                                                                                                  Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ24330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-3'; exonuclease; PCR; amplification; SSR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase enzyme MET-LEU 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR23170;
                                                                                                                                                                                                                                                                                                                                                                                                       Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9206200-A.
                            See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 LSKRIGLSVSE 658
                                                                                                                                                                                                                                                                                                                                                                          1992-150885/18.
856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Gelfand
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                900S-0590466
900S-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0590213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residues 2-27 deleted from the native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                       DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing; PLCR
                                                                         recombinant
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RESULT 9
AAR23122
ID AAR2
                                                                            В
                                                                                                        δÃ
                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
AAR23122 standard; Protein; 892 AA
                                                                                                                                                                                                                                                             nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinantesis having 5'-3' exonuclease activity to a complete lack of proteins having 5'-3' exonuclease activity to a complete lack of proteins having 5'-3' exonuclease activity to a complete lack of proteins having 5'-3' exonuclease activity to a complete lack of proteins and proteins are proteins.
                                                                                                                                                                                                                                                                                                           polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a mutant of Thermosipho africanus polymerase nutant ASP37 Taf, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nucleativity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant thermostable DNA polymerase enzyme ASP37 Taf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR23169 standard; Protein; 892 AA
                                                                                                                                                                                                                                   See also AAR23140-79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09206200-A
                                                                            740 LSKRIGLSVSE 750
                                                                                                          1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RD,
                                                                                                                                                                                                     892 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gelfand.DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-US07035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Gly in native sequence"
                                                                                                                                                      100.0%;
                                                                                                                                         0;
                                                                                                                                                      Score 49; DB 1:
Pred. No. 0.18;
                                                                                                                                         Mismatches
                                                                                                                                                                      DB 13;
                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                          An enhanced amt. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exo nuclease
                                                                                                                                                                     Length 892;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for use
                                                                                                                                                                                                                                                                               recombinant
                                                                                                                                       0;
                                                                                                                                       Gaps
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                                                                                                                                                                                                              AAY65382
                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase activity, reverse transcriptase activity, and opt. 5'-3' and/or 3'-5' exonuclease activity. The Taf enzyme does not become irreversibly denatured for relatively short exposures to temperatures of 90-100 deg.C. The Taf enzyme has an optimum temperature above 45 deg.C and exhibits activity over a broad temperature range of 37-90 deg.C. The Taf polymerase is suitable for use in PCR and in other techniques such as DNA sequencing, nick-translation and reverse transcription.
                                                          Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensi; location; development; protein synthesis; stability;
                                                                                                             Human 5' EST related polypeptide SEQ ID NO:1543.
                                                                                                                                            01-FEB-2000 (first entry)
                                                                                                                                                                                               AAY65382 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 68; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable DNA polymerase from Thermosipho africanus - propd. by purificn. from cells or by expression of Taf polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostability; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taf DNA polymerase I.
                       Homo sapiens.
                                                                                                                                                                        AAY65382
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The thermostable polymerase from Thermosipho africanus (Taf) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ23917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-150887/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09206202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermosipho africanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR23122;
                                                  regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in host cells
                                                                                                                                                                                                                                                                  740 LSKRIGLSVSE 750
                                                                                                                                                                                                                                                                                           1 LSKRIGLSVSE 11
                                                                                     5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                  AAQ23918-Q23961.
                                                                                                                                                                                                                                                                                                                                                                          892 AA;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91WO-US07076
                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exonuclease; proofreading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenfield L,
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                Score 49; DB 1
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawyer FC,
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                            Length 892;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reichert FL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                    Gaps
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W09953051-A2

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RESULT 11
AAB43412
ID AAB43
XX AB43
AC AAB43
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ42265 .o AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAX64651 to AAX64538 represent the EST-related proteins corresponding to AAZ42265 to AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in organization of a contraction of a contraction between the protects. The nucleic acids encoding signal peptides can be used for distraction activation be
                                                      immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                  Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; notropic;
                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated protein sequence SEQ ID NO:857
                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1998;
28-APR-1998;
                              neurological disease; drug screening
                                                                                                                                                          vasotropic; antipsoriatic; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB43412 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 815; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel secreted protein 5' expressed sequence tag sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-038446/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0057719
98US-0069047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 128;
                                                                                                                                                          gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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XX
                                                                                                                                                                                                                                                                                 antidiabetic; antiashmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating cameliorating medical conditions and diagnosing pathological conditions.
                                                           inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. ARC78449 to ARC78457 and AAB44240 represent sequences used in the exemplification of
Sequence
                                                                                                                                                                            immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ
                                                                                                                                                                                                                                           Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                           the present invention.
                                                                                                                                                       rejection, modulate haemostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                     or inhibiting the proliferation, differentiation or mobilisation of
                                                                                                                                                                                                                                                                                                                                                                                                                       include: cytostatic; proliferative; vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                             in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities {\sf tissues}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC77607 to AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 1411-1412; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding poptides useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC77621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,21-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM
258 AA;
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                                                                                                                                                                                                                                                                                                                treating or
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AAR79585
                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                         Matches 8; Conserv
                                                                            17-JUL-1996 (first entry)
murine; denaturation; renaturation.
        Chaperonin containing TCP-1; CCT; subunit; protein folding complex;
                                          Mouse CCT-theta subunit sequence, deduced from clone pTthetal.
                                                                                                                AAR79585;
                                                                                                                                          AAR79585 standard; Protein; 548 AA
                                                                                                                                                                                                                             148 RIGLSVSE 155
                                                                                                                                                                                                                                                          4 RIGLSVSE J1
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                        Score 36;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                      DB 21;
. 23;
                                                                                                                                                                                                                                                                                                                       Length 258;
                                                                                                                                                                                                                                                                                       indels
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                                                                                                                                                                                                                                                                                    Caps
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0,

03-AUG-1995.

Mus musculus

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RESULT 13
AAYO7062
ID AAYO7
XX
AC AAYO7
XX
DT 02-JI
XX
DE Rena
XX
Canc
KW Canc
KW bres
KW bros
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Hom
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PN W09
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PN 809
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PD 28-
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YR 10
PR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
     22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                 Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; qastric cancer: renal cancer: line o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney cDNA library during a screen for ion transport channel genes. TCP-1 and the proteins encoded by the cDNA clones are individual subunits of a heteromeric chaperonin which has been designated "chaperonin, containing TCP-1" (CCT). The chaperonin acts as a protein folding complex. The present sequence is that of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human pr bes recovered by PCR of human HT1080 cell line cDNA using degenerate primers from a conserved region of TCP-1 and TF55. Clone pCBL80 was isolated during a mouse testis CDNA sequencing project and clone pTgamma7 was recovered by hybridisation with a mouse cDNA PCR product which was made with primers derived from the sequence of a TCP-1 related gene fragment recovered accidentally from a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse cDNAs encoding novel TCP-1-related proteins were isolated using a combination of methods. Clones prdelta2 and pTzetal2 were isolated by cross-hybridisation with C.elegans cDNA probes recovered from a 5'-expressed sequence tag collection. The clones pTbeta2, pTepsilon5 and pTthetal were isolated by cross-hybridisation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1994;
31-JAN-1994;
                                                                                                                                                                                                                                      WO9904265-A2
                                                                                                                                                                                                                                                                                                                                           prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Renal cancer associated antigen precursor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY07062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY07062 standard; Protein; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Fig 4; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Folding protein complex sub-unit(s) - with ability to form complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-1995;
                                                                                                                                   15-JUL-1998;
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vitro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashworth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CANC-) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 RIGLSVSE 127
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-275439/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in facilitating folding of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANCER RES ROYAL CANCER HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kubota H,
     98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
                                                                                                                                                                                                                                                                                                                                                              colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94GB-0018234.
94GB-0001791.
                                                                                                                                   98WO-US14679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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# ABG21964
.. XX
AC ABG2
XX
AC ABG3
XX
DT 18-1
XX
NOVE
XX
NOVE
XX
KW Huma
KW FOOO
XX
OS Home
XX
PD 11--
XX
PF 30--
XX
PF 31--
PR 23--
XX
PR 24--
XX
PR 24-
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  N-PSDB; AAS86151.
                          WPI; 2001-639362/73
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
Drmanac RT, Liu C,
                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG21964 standard; Protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 458-459; 787pp; English
                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #21955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2002 (11rst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG21964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
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11-OCT-1997;
                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RIGISVSE 11
                                                                                                                                                                                                                                                                                                                                                                                             chromosome mapping; gene mapping; gene therapy; forensic
upplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conserv
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97GB-0021697.
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Sahin
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100.0%; Prr
Tang YT;
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Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                         forensic;
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RESULT 15
ABG21966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; torensic; food supplement; medical imaging; diagnostic; genetic disorder.
New isolated polynucleotide and encoded polypeptides, useful in
                                      N-PSDB; AAS86153
                                                                                        Drmanac RT, Liu C,
                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG21966 standard; Protein; 584 AA
                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #21957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (II) sequences. (I)
polymerase chain reaction (PCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 52323; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biddings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides are also used in diagnostics as expressed sequence tags
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127 RIGLSVSE 134
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                                                         2001-639362/73
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8; Conserv
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                                                                                        Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 555; 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                              diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                              polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity \,\cdot\,
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 52325; 103pp; English
584 AA;
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Search completed: January 15, 2003, 11:20:21 Job time: 32.2857 secs

DЪ γ

108 RIGLSVSE 115

Query Match Best Local S Matches 8

Local Similarity hes 8; Conserv 4 RIGLSVSE 11

Conservative

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Gaps

0;

73.5%;

Score 36; DB 22; Pred. No. 57; Mismatches

Length 584; Indels

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

4, Appli 5073, Ap 13, Appl 2, Appli 56, Appl 56, Appl

Sequence Sequence Sequence

1, Appli 9, Appli 2, Appli 2, Appli 2, Appli 2, Appli 2, Appli Sequence Sequence Sequence Sequence Sequence

29, Appl 27, Appl 29, Appl 29, Appl 29, Appl

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
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49
        Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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        DВ
    US-07-977-434-12
US-08-48-819-12
POT-US91-07035-12
US-08-687-590-31
US-08-687-590-31
US-09-58-687-591
US-09-199-637A-13
US-08-780-749A-6
US-08-780-749A-6
US-08-790-7231-16
US-09-797-231-16
US-08-70-511-6
US-08-870-511-10
US-08-870-511-12
US-08-70-511-12
US-08-70-511-12
US-08-70-511-12
US-08-70-511-12
US-08-70-511-12
US-08-70-511-12
US-09-134-001C-3866
US-08-564-972-8
US-09-514-972-8
US-09-514-972-8
US-09-514-972-8
US-09-514-972-8
US-08-148-0588-29
US-08-148-0588-29
US-08-478-042-27
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(without alignments)
34.855 Million cell updates/sec
 Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 27, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 34, Appl Sequence 3666, Ap Sequence 37, Appl Sequence 3866, Ap Sequence 37, Appl Sequence 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                              Patent No
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US-07-977-434-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPorfect 2.1
CURRENT APPLICATION DATA:
FILING DATE: 22-AUG-19
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US
FILING DATE: 15-AUG-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 28-SEP-19
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 28 SEP-
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APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17-JUN-
FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-JAN-
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5:
FILING DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD...
STREET:
STREET:
Nutley
New J
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 590,213 FILING DATE: 28-SEP-1990
                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12, Application US/07977434
o. 5466591
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07110-1199
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                   15-AUG-1991
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                                                                                                                           US 063,509
                                                                                                                                                                       US 143,441
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                                                                                                                                                                                                                                                                                                              US 590,466
                                  US 746,121
                                                                             US 899,241
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US-08-645-215-27
US-08-645-215-29
US-08-665-604-29
US-08-466-604-29
US-08-4737-716-4
US-09-134-001C-5073
US-09-134-016-2
US-09-186-1888-56
US-09-186-1888-56
US-09-186-1988-56
US-09-186-1988-56
US-09-186-1988-56
US-09-186-1988-56
US-09-186-1988-56
US-09-186-1988-56
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US-09-186-1988-56
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US-08-216-971-2
US-08-812-979-2
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Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 892 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: Car
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: US 455,611
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                       APPLICATION NUMBER: US 590,466 FILING DATE: 28-SEP-1990
                                                                                                      APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990
        FILING DATE:
                                                                                                                                       APPLICATION NUMBER: 07/9;
FILING DATE: 23-FEB-1993
                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                            CITY: Nutley
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                        APPLICATION NUMBER:
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07110-1199
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имвек: US 590,213
28-SEP-1990
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24-JUL-1990
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US-08-458-819-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 49; DB 1; Best Local Similarity 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ 11) NO: SEQUENCE CHARACTER(STICS:
                                                                                                                                                                                         APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                               STATE: LL 94608
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APPLICATION NUMBER: US 523,394
                                                                                                                                                                                                                                                                                                                                                                                       740 LSKRIGLSVSE 750
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.0
                                                                                                                               CITY:
                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                             ADDRESSEE:
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                                                        MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                         Emeryville
: California
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                                                                                                                                        1400 Fifty-third Street
                                                                                                                                                             Cetus Corporation
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                                                    Floppy disk
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RESULT 4
US-08-687-590-31
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                                          Sequence 31, Application US/08687590 Patent No. 6255070 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
            APPLICANT: Willison, Keith Robert APPLICANT: Kubota, Hiroshi
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 892 amino acid
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PC
                                                                                                                                                             740 LSKRIGLSVSE 750
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                                                                                                                                                                                                                                                                                                                                           AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                            892 amino acids
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                                                                                                                                                                                                                                            100.0%; Score 49; DB 5; 100.0%; Pred. No. 0.022;
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US-08-905-223-272
                                                                                                                                                                                                                                                                                                                                         Sequence 272, Application US/08905223 Patent No. 6222029
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CURRENT APPLICATION DATA:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                APPLICANT: Edwards,
APPLICANT: Duelert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
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                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RIGLSVSE 127
                                DEPTHARE: WORD

OPERATING SYSTEM: Win95
SOFTWARE: WORD
                                                                                                                        COUNTRY: USA
ZIP: 92101-3505
                                                                                                                                                          CITY: San Diego
STATE: Californ
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/OFILING DATE: 31-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                        California
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                                                                                                                                                                                  501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548 amino acids
                                                                                                                                                                                                                                              Lacroix, Bruno
VENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashworth, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Townsend and Townsend and Crew LLP
                                                                                                                                                                                                        Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%; Score 36; DB 4; Length 548; 100.0%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                       Aymeric
                                                                                                                                                                                                                                                                                                       Jean-Baptiste D.
                                                                                                                                                                                                                                           503
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Indels

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Matches Query Match

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RESULT 7
US-09-199-637A-13
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US-09-586-875-1
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US-09-586-875-1
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               Sequence 13, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                              Query Match 69.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09586875 Patent No. 6385546
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kath, Peter C.
APPLICANT: G. dman, Adrian
APPLICANT: Helin, Sari
TITLE OF INVENTION. STRABILIZING AND DESTABILIZING PROTEINS
FILE REFERENCE: 08036-018002
CURRENT APPLICATION NUMBER: US/09/586,875
CURRENT FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 08/971,004
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/030,926
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                          ENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                           118 KRLGLPVSE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.4%; Score 34; DB 4; Length 79; Local Similarity 63.6%; Pred. No. 2.4; hes 7; Conservative 2. vicini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 10.8 OTHER INFORMATION: seq VLLFFVLLGMSQA/GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 LAKTLGLEVSE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                              3 KRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSKRIGLSVSE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 79 amino acids
AMINO ACID
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                                                                                                                                                                                                                   Score 34; DB 4;
Pred. No. 15;
                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                    Length 373;
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; TYPE: PRT
; ORGANISM: PSeudomonas acruginosa
US-09-199-637A-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/199,637A CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,517 PRIOR FILING DATE: 1997-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: VIBULENCE ASSOCIATED NUCLEI
TITLE OF INVENTION: SEQUENCES AND USES THERROF
FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
 SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acid
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Huszat, Dennis
APPLICANT: Wei, Gu
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656 LAKREGLSV 664
                                                                                                                       NAME: COTUZZÍ, LAUTA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7853-060
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/662,560 FILING DATE: 10-JUN-1996
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: NY
                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
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332 amino acids
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                                                                                                                                                                                                                                                                                                                                  SYSTEM: DOS
FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                             10-JUN-1996
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77.8%;
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Pred. No. 84;
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US-08-706-281A-16
: Sequence 16, Application US/08706281A
; Patent No. 6100048
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; FRAGMENT TYPE:
US-08-662-560-2
                                             RESULT 10
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                                                                                                                                               Matches
                                                                                                                                                                         Query Match
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Matches 5; Conserva
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                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/780,749A
FILING DATE: 08-0AN-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREEN
TITLE OF INVENTION: USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                     ||:|:|:|
164 KRVGISIS 171
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                                                                                                                                            Local Similarity tes 5; Conserv
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                                                                                                                  3 KRIGLSVS 10
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                    (212) 790-9090
(212) 869-8864/9741
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internal
                                                                                                                                                         65.3%;
62.5%;
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62.5%;
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                                                                                                                                             3; Mismatches
                                                                                                                                                           Score 32; DB 2;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                7853-064
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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RESULT 11
US-09-097-231-16
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                                                                                                                                                                                                                                                                     Sequence 16, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
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Matches 5; Conserv
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OPERATING SYSTMM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagoni
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/OFILING DATE: 04-SEP-1996
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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                    Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
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                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Pred. No.
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APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: GU, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT
FILE REFERENCE: 7883-083
CUURRENT APPLICATION NUMBER: US/08/870,511
CUURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
NUMBER OF SEQ ID NOS: 45
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                 Sequence 8, Application US/08870511 Patent No. 6287763
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Best Local Similarity
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         APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT
FILE REFERENCE: 7853-083
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CURRENT APPLICATION NUMBER: US/08/870,511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
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Pred. No.
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, RESULT 15
US-08-870-511-12
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Best Local Similarity 02...
Watches 5; Conservative
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                                                                     ; ORGANISM: Homo sapiens US-08-870-511-12
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; Patent No. 6287763
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 332
                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 332
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SEQ ID NO 10
LENGTH: 332
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Best Local Similarity
Matches 5; Conserv
Query Match 65.3%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ 1D NOS: 45
                                                                                                                                                                                                                                                                                  APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
                                                                                                                                                                                                                               TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE TITLE OF INVENTION: REGULATION OF BODY WEIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/870,511 CURRENT FILLING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GU, Wei TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE TITLE OF INVENTION: REGULATION OF BODY WEIGHT FILE REFERENCE: 7853-083
                                                                                                                                                                                                                        FILE REFERENCE: 7853-083
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Score 32; DB 4; Pred. No. 36; 3; Mismatches
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Pred. No.
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3 KRIGLSVS 10 ||:|:|:| 164 KRVGISIS 171

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Search completed: January 15, 2003, 12:38:25 Job time: 10.2857 secs

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Sequence 11, Sequence 5404, Ap Sequence 12578, A Sequence 12778, A

Appl

Sequence

47352, A 7, Appli

Sequence 97, Appl
Sequence 341, Appl
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 374, App
Sequence 374, App
Sequence 311, App
Sequence 319, App
Sequence 319, App
Sequence 302, Appli
Sequence 316, Appl
Sequence 319, Appl

Sequence 139, Appl Sequence 78, Appl Sequence 78, Appl Sequence 5824, Ap Sequence 5458, Ap

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Minimum DB .
Maximum DB .
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Perfect score:
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             \begin{array}{c} \mathbf{4} & \mathbf{6} & \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein search, using sw model
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length: 2000000000
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                                  Match
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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10 US-09-823-649A-17
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10 US-09-98-031A-2
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10 US-09-98-19-242-10980
10 US-09-815-242-10980
10 US-09-815-242-1087
         US-09-815-242-5520
US-09-815-242-12367
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US-09-867-550-482
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      Sequence 44, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 6454, Ap
Sequence 4, Appli
Sequence 15520, Ap
Sequence 12367, Ap
Sequence 12384, A
Sequence 482, App
                                                                                                                                                                                                        Sequence 2, Appli
Sequence 9, Appli
Sequence 6, Appli
Sequence 10980, A
Sequence 4, Appli
Sequence 5030, Ap
Sequence 5030, Ap
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                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Appli
Sequence 17, Appl
Sequence 857, App
; Patent NO. VECULE:
                                US-09-823-649A-17

: Sequence 17, Application US/09823649A

: Patent No. US20020012970A1
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US-09-823-649A-6
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Smith, Edward
APPLICANT: Elistrom, Carita
APPLICANT: Gelfand, David
APPLICANT: Higuchi, Russell
APPLICANT: Myers, Thomas
APPLICANT: Schoenbrunner, Nancy
APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
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                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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US-09-908-931B-11

US-09-815-242-12578

10 US-09-815-242-12578

10 US-09-815-242-12778

US-09-91-932-97

12 US-09-907-824-341

US-09-907-824-341

US-09-907-841-341

US-09-907-841-341
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US-10-051-643-78
US-09-880-505-78
US-09-738-626-5824
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                                                                                                                                                           Sequence 2, Application US/08808031A Patent No. US20020048802A1
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                         GENERAL INFORMATION:
APPLICANT: Inouye, Sumiko
APPLICANT: Hsu, Mei-Yin
APPLICANT: Eagle, Susan
APPLICANT: Inouye, Masayo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,301 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21
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                APPLICANT: Inouye, Masayori
TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 52
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                 148 RIGLSVSE 155
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les 8; Conserv
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Elfstrom, Carita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang, Alice
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Schoenbrunner, Nancy
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                              73.5%; Score 36; DB 10; Length 258; 100.0%; Pred. No. 5.5;
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US-09-214-474A-6
                    RESULT 6
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Query Match
Best Local Similarity
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                                                                                                                                ; TYPE: PRT; ORGANISM: Streptococcus salivarius US-09-981-900B-9
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                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ 1D NO 9
LENGTH: 822
                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09981900B Patent No. US20020138878A1
                                                                  Matches
                                                                                                                                                                                                                                                      TITLE OF INVERVION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH DEG TITLE OF INVERVION: AND CELLULOSE TO FERMENTABLE SUGARS FILE REFERENCE: MSU 4.1-539

CURRENT APPLICATION NUMBER: US/09/981,900B

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 60/242,408
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
APPLICANT: Dale, Bruce E
                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 1D NO: 2:
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LENGTH: 485 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 37.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPHAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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   63
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REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 03-MAI
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                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: WEISER & ASSOCIATES STREET: 230 South Fifteenth Street, Suite 500
                                2 SKRIGLSVSE 11
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SKRAGLSVED
                                                                 Similarity 7; Conserv
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70.0%;
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                                                                              Score 33; DB 10;
Pred. No. 78;
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Pred. No. 28;
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                                                                                              Length 822;
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US-09-815-242-10980
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; ORGANISM: Streptococcus pneumoniae
US-09-214-474A-6
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SEQ ID NO 6
LENGTH: 112
                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10980
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Best Local :
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CURRENT FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: US 60/057,520
PRIOR FILING DATE: 1997-09-04
PRIOR APPLICATION NUMBER: PCT/US98/18291
PRIOR FILING DATE: 1988-09-03
                                                                                                                                                                                                                                                                                                                                                                                                CUKKENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: BL'TRA.011A
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                          PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Chappell, Amy M.
TITLE OF INVENTION: NO. USZ0020049311A1el Rnase P
FILE REFERENCE: GM50036
                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                 PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-23
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                 ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,848
                                                          LENGTH: 146
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nes 6; Conserv
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Carr, Grant J.
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75.0%;
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Pred. No. 22;
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US-09-815-242-5030
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 54.5%;
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                                                                                                                                                                                                               CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith &
APPLICANT: Wall, Daniel
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TITLE OF INVENTION: 45508, A NOVEL HUMAN PEPTIDYL-TRNA
TITLE OF INVENTION: HYDROLASE FAMILY MEMBER AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/213,688 PRIOR FILING DATE: 2000-06-23
                                 PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                               PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                        PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                FILE REFERENCE:
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PRIOR APPLICATION NUMBER: 60/269,308
                   PRIOR FILING DATE:
                                                                                                                                       PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
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Xu, H. Howard
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Pred. No.
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RESULT 11
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           Sequence 44, Application US/10027806 Patent No. US20020160476A1 GENERAL INFORMATION:
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LENGTH: 201
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APPLICANT: Swanson, Ronald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-05-26
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PRIOR TILING DAYE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/2006,848
PRIOR RILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/257,931
                                                                                                                            VSRRLGISLS 20
                                                                                                                                                                                            Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind, Judith W.
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                           63.3%;
50.0%;
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50.0%;
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Pred. No.
                                                                                                                                                                                                                          Score 31;
                                                                                                                                                                                                             Pred. No.
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41;
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US-08-808-031A-42
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                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Cenarchaeum symbiosum US-10-034-623-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-034-623-44
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                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                        APPLICANT:
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                       255 KRIGLKVID 263
                                                                                                                         Hsu, Mei-Yin
                                                                                                                                        Inouye, Sumiko
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Best Local Similarity
Matches 6; Conserv
Publication No. US20020198365A1
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A CURRENT APPLICATION NUMBER: US/10/027,806 CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feldman, Robert A. APPLICANT: Schleper, Christa
                                                                                                                                                                                                                                                                                                                       ORGANISM: Cenarchaeum symbiosum
                                                                                                                              255 KRIGLKVTD 263
                                                                                                                                                                    3 KRIGLSVSE 11
                    Application US/10034623
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                 63.3%;
66.7%;
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                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                             0;
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APPLICANT: Feldman, Robert A. APPLICANT: Schleper, Christa APPLICANT: Swanson, Ronald V.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A CURRENT APPLICATION NUMBER: US/10/034,623 CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: 60/102,294 PRIOR FILING DATE: 1998-09-29 PRIOR APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: 1999-09-29 SOFTWARE: FastSEQ for Windows Version NUMBER OF SEQ ID NOS:

Query Match Best Local Similarity 3 KRIGLSVSE 11 6; Conservative 66.7%; Score st; DB Pred. No. 67; Mismatches Length 310; Indels 9 Gaps 0;

; Sequence 42, Application US/08808031A
; Patent No. US20020048802A1

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia Eagle, Susan

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Query Match
Best Local Similarity
7; Conserva
                                                                                   ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-808-031A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-738-626-6454
                                                                                                                                                      SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMA ON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6454, Application US/09738626
Publication No. 7S20020197605A1
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Best Local :
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                       PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSH
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                        LENGTH: 526
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LENGTH: 480 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 LAKALGISVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 03-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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les 6; Conserv
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                  SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOKOI, HARUHIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIZOGUCHI, HIROSHI
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                  Conservative
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                score 31; DB 9; Length 526;
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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                                                                                                                                                        ; ORGANISM: Homo sapiens US-09-999-248-4
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                                                  Query Match
Best Local Similarity 70.0
Varches 7; Conservative
                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09999248 Patent No. US20020176852A1
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/289,172
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/289,537
PRIOR FILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cheng, Guangjie
TITLE OF INVENTION: Mitogenic Oxygenase Regulators
FILE REFERENCE: 05501-0180 43150-266489
CURRENT APPLICATION NUMBER: US/09/999,248
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/249,305
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/251,364
PRIOR ETLING DATE: 2000-12-05
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lambeth,
                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                 ENGTH: 565
232 LEKAIGLAVS 241
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                                    1 LSKRIGLSVS 10
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                                                                                             63.3%;
70.0%;

    Mismatches

                                                                                           Score 31; DB 9;
Pred. No. 1.3e+02;
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Search completed: January 15, 2003, 12:39:52 Job time: 11.8571 secs

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Result
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Maximum DB seq
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Perfect score:
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 protein search, using sw model
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49
1 LSKRIGLSVSE 11
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Match
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 283224 seqs, 96134422 residues
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compug
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pir4:*
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 DВ
119599

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## ALIGNMENTS

RESULT H64428

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbock, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Mcthanococcus jannasc A;Reference number: A64300; MUID:96337999; PMID:8688087

maggresium and cobalt transport protein homolog - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999 C;Accession: H64428

A; Reference number: A; Accession: H64428

A; Molecule type: DNA A; Residues: 1-317 <BUL>

A; Status: preliminary; nucleic acid sequence not shown; translation

not shown

A;Map position: FOR965089-966042 C;Superfamily: magnesium and cobalt transport protein

A;Cross-references: GB:U67546; GB:L77117; NID:g1591687; PIDN:AAB99037.1; PID:g1499876 C;Genetics:

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Query Match	A; Introns: 64/3; 94/1; 214/3	A; Gene: CESP:C31A11.9 A: Map position: 5	C; Genetics:	A; Experimental source: clone C31A11	A;Cross-references: EMBL:Z83218; PIDN:CAB05691.1; GSPDB:GN00023; CESP:C31A11.9	A; Residues: 1-352 <wil></wil>	A; Molecule type: DNA	A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Accession: T19599	A; Reference number: Z19149	submitted to the EMBL Data Library, December 1996	R;McMurray, A.	C; Accession: T19599	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999	C; Species: Caenorhabditis elegans	hypothetical protein C31A11.9 - Caenorhabditis elegans	T19599	RESULT 2		,	Db 44   SKKTGTSVSD 5.3	KY F ESPARACESASE II		٠,	Rest [OCA] Similarity	);;;;; <b>K</b> )+
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Length 352;					GSPDB:GN00023;		•	-					,	<pre>#text_change 1</pre>	•	gans								0; Indels	Length 31/;	1
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A; Accession: C97063
A; Accession: C97063
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-285 <KUR>
A; Cross-references: GB: AE001437; PIDN: AAK79294.1: PIE
A; Experimental source: Clostridium acetobutylicum ATC
C; Genetics:
A; Gene: CAC1325
C; Superfamily: conserved hypothetical protein yitT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.C A;Title: The complete genome sequence of the gastric pathogen Helicobacter A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uncharacterized conserved protein, YitT (B. subtilis) family CAC1325 [imported] - C.Species: Clostridium acetobutylicum c.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C.Accession: C97063 R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000536;
C;Superfamily: shikimate kinase;
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C;Date: 09-Aug-1997 *sequence_revision 09-Aug-1997 *text_change 18-Jun-1999
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muconate cycloisomerase I PA2509 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
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R; Stover, C.K.; Pham, X.O.; adman, S.; Yuan, Brody,
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C;Superfamily: mucon
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A; Residues: 1-373 <STO>
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A; Residues: 1-116 <S
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A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: C86120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C;Accession: JC4073; PC4022; S52867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE004678; GB:AE004091; NID:g9948560; PIDN:AAG05897.1; GSPDB:GN
A;Experimental source: strain PAO1
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                                                                               C;Accession: C86120
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                     probable growth inhibitor [similarity] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The eighth Cct gene, Cctq, encoding the theta subunit A; Reference number: JC4073; MUID:95197008; PMID:7890169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: This protein is involved in folding, transport
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                                                     A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
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gasawara,
                                      R;Hayashi,
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C;Accession: C91279
                                                                                             probable growth inhibitor [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
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C;Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97122.1; PID:g537067
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Burland, V, Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blatt Nucleic Acids Res. 23, 2105-2119, 1955
A;Tille: Analysis of the Esohefichia coli genome VI: DNA sequence A;Reference number: S56314; MUID:95334362; PMID:7610040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Masuda, Y.; Miyakawa, K.; Nishimura, Y.; Ohtsubo, J. Bacteriol. 775, 6850-6856, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell growth regulatory protein ChpBK - Escherichia coli (strain K-12) M;Alternate names: pemk-like protein 2 C;Species: Escherichia coli C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 01-Ma C;Accession: D49339; S56451; D65234
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A;Experimental source:
C;Genetics:
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A; Residues: 1-116 <BLAT>
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A; Residues: 1-116 <MAS>
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N.; Yasunaga, T.; Kuhara,
8, 11-22, 2001
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                                      T.; Makino, K.; Ohnishi,
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                    Shiba, T.; Hattori, M.; Shinagawa,
                                        Kurokawa, K.; Ishii, K.;
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RESULT 11
RGECLR
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C; Superfamily:
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A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamo, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A69580; MUID:98044033; PMID:9384377
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A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galiz iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, A.; Liu, H.; Mass, A.; Luthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mass, A.; Luthors, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mass, A.; Luthors, C.; Luthors, A.; L
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: An Irp-like game of Bacillus subtilis involved in branched-chain amino acid A; Reference number: Z2287; MUID:974;1495; PMID:9287000 A; Accession: T44776
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
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A; Residues: 1-157 < KUN>
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A; Residues: 1-116 < HAY>
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A; Residues: 1-157 <BEL>
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                                                                                                  1 LSKRIGLSVS 10
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LSKKIGLSPS 36
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8; Conser
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80.08;
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Pred. No.
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15;
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A;Cross-references: GB:M35869; NID:gl46664; PIDN:AAA24089.1; PID:gl46665  
R;Ito, K.; Kawakami, K.; Nakamura, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 302-306, 1993
A;Title: Multiple control of Escherichia coli lysyl-tRNA synthetase expression A;Reference number: I59240; MUID:93126364; PMID:7678344
A;Accession: I59240
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A;Title: Characterization of Lrp, an Escherichia coli regulatory protein that mediates
A;Reference number: JH0412; MUID:91250369; PMID:2040596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: regulatory protein asnC C;Keywords: DNA b'ding; homodimer; transcription regulation F;2-164/Product: 1-xcine-responsive regulatory protein #statur;30-56/Region: hexix-turn-helix motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64827
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                   F;30-56/Region:
                                      C; Superfamily: regulatory protein asnC C; Keywords: DNA binding; transcription
                                                                                       A; Description:
                                                                                                                C; Function:
                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-164 < CAL>
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                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S59991
                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Serratia marcescens
C;Date: 15-Feb-1996 #sequence_1
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A;Cross-references: GB:D11105; NID:g216585; PIDN:BAA01880.1; PID:g216586
A;Cross-references: GB:D11105; NID:g216585; PIDN:BAA01880.1; PID:g216586
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A;Residues: 1-164 <RES>
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A; Residues: 1-164 <WIL>
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                                                                                                                                                                                      A;Cross-references: EMBL:U02276; NID:g407920; PIDN:AAA75466.1;
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                                                                                       activates a number of operons in response
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                        helix-turn-helix motit
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87.5%;
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R;Calvo, J.M. Submitted to the EMBL Data Library, September 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription regulator |rp, |eucine-responsive - Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 26-Aug-1C;Acces-ion: S59992
                                                                                                                                           A:Description: activates a number of operons in response C;Superfamily: regulatory protein asnC C;Keywords: DNA binding; transcription regulation F;30-56/Region: helix-turn-helix motif
                                                                                                                                                                                                                                                                         A;Cross-references: EMBI::U02274;
A:Note: the source is designated
                                                                                                                                                                                                                                                                                                                                                                                        A; Description: The amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: DNA
F; 30-56/Region:
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A; Residues: 1-164 < CAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: The amino acid sequence of Lrp (leucine-responsive regulatory protein) A; Reference number: 859991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Salmonella typhimurium
C;Date: 15-reb-1996 #sequence_revision 01-Mar-1996 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                   A; Residues: 1-164 <CAL>
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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A;Cross-references: GB:AE004266; GB:AE003852; NID:g9656435; PIDN:AAF95052.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1904
A;Map position: 1
C;Superfamily: regulatory protein asnC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B82142
| Leucine-responsive regulatory protein VC1904 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82142
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A;Molecule type: DNA
A;Residues: 1-164 <HEI>
Search completed: January 15, 2003, 12:37:27 Job time: 16.1429 secs
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Best Local Similarity
Matches 7; Conserv
                                                                                                          1 LSKRIGLS 8
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34 LSKRVGLS 41
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Minimum DB seq Maximum DB seq

length: 0 length: 2000000000

Searched:

Scoring table: Sequence: Title: Perfect score:

US-09-823-649A-6 49

1 LSKRIGLSVSE 11

Run on: OM protein -

protein search, using sw model

GenCore version 5.1.3 Compugen Ltd.

January 15, 2003, 09:04:22; search time 6.28571 Seconds (without alignments) 72.584 Million cell updates/sec

Database

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Matches 7; Conserv
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"The DNA sequence of human chromosome 21 "."
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T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta).
CCT8 OR CCTQ OR KIAA0002.
                                                                                                                     cytosolic chaperonin containing TCP-1.";
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                           Kubota H., Hynes G., Willison K.; "The eighth Cct gene, Cctq, encoding the theta subunit of the
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                                                                                                        Gene 154:231-236(1995).
                                                                                                                                                                                       MEDLINE~95197008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96127533; PubMed=8590283; Yamazaki M., Ono A., Watanabe K.,
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                                                                                                                                                                                                                                                                        "The DNA sequence of human chromosome 21.";
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                   ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING ACTIN AND TUBULIN.
SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT
                                                                                FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
    FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER
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40, Last sequence update)
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation
                                                                              -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
-1- SUBCELLULAR LOCATION: CYTOPlasmic.
                                                                                                                                                                                       "The eighth Cct gene, Cctq, encoding the theta subunit of the cytosolic chaperonin containing TCP-1.";
                                                                                                                                                                                                                                         MEDLINE=95197008; PubMed=7890169;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                             T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta). CCT8 OR (CCTQ.
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 01-NOV-1995 (Rel. 01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                          P42932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chaperone; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00750; TCP1_1; 1. PROSITE; PS00751; TCP1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00298; CHAPERONIN60. PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00118; cpn60_TCP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                          Kubota H.,
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:1623; CCT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ICPO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 8; Conserv
                                                                                                                                 WE 154:231-236(1995).

FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON AUP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF ACTIN AND TUBULIN.
                                                                   SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
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AL163249; CAB90433.1; -.
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IPR001844; Chaprnin_Cpn60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 AA;
                                                                                                                                                                                                                         Hynes G., Willison K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                     32, Created)
32, Last sequence update)
33, Last annotation update)
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A -> V (IN REF. 1).
566A6622BC2D15E9 CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
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15-JUN-2002
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Alanyl-trNA $
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furlosus genome.",
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AITH + L-alanine + tRNA(Ala) = AMP +
diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELIULAR LOCATION: Cytoplasmic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
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Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Aminoacyl-tRNA synthetase; Protein biosyntl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8U425;
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                                                                                317 VAKRYGISVEE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 RIGLSVSE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                         1 LSKRIGLSVSE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE010151; AAL80394.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P48424; 1A6D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z37164; CAA85521.1; -.
                                                                                                                                                                                                                                     Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           proteome
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                                                                                                                                                                                                                                                                                                                                                                                           914 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last anotation update)
synthetase (EC 6.1.1.7) (Alanine--tkNA ligase) (AlakS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%; Score 36; DB 1; Length 548; ilarity 100.0%; Pred. No. 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           104906 MW; 467F593731BD8BC1 CRC64;
                                                                                                                                                                                                                                                                          73.5%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                         Pred. No. 31;
4; Mismatches
                                                                                                                                                                                                                                                                                                                  Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4B5265250CFF1FE2 CRC64;
                                                                                                                                                                                                                                                                                                                  DB 1; Length 914;
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        DRA REPERENCE COCCOCCOCCE PERENCE REPERENCE RE
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CHPB_ECOLI
EcoGene; EG12096; chpB.
InterPro; IPR003477; PemK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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modified and this statement is not removed. Usage by and for common entitles remittee a line of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacter101. 176:5861-5863(1994).

-I- FUNCTION: MAY HE INVOLVED IN THE REGULATION OF CELL GROWTH.
AS A GROWTH INLIBITOR. BOTH CHPS AND CHPB BIND TO THE PROMOREGION OF THE CHPS BOTHON TO AUTOREGULATE THEIR SYNTHESIS.
-I- SIMILARITY: BELONGS TO THE PEMK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence up
16-007-2001 (Rel. 40, Last annotation
PemK-like protein 2.
2) PDB OR Curve.
EMBL; D16451; BAA03920.1; -- EMBL; M14018; -- NOT_ANNOTATED_CDS.
EMBL; U14003; AAA97122.1; -- EMBL; AE000494; AAC77182.1; -- EMBL; M23550; -- NOT_ANNOTATED_CDS.
PIR; D49339; 149339.
                                                                                                                                                                                                                                                                                                      This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heinonen J.; "Cloning and characterization of the gene encoding inorganic nyrophosphatase of Mscherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE~95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masuda Y., Miyakawa K., Nishimura Y., Ohtsubo E.; 
"ChpA and ChpD, Escherichia coli chromosomal homolog 
locus responsible for stable maintenance of plasmid 
J. Bacteriol. 175:6850-6856(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHPB OR CHPBK OR H4225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHPB
                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weiss D.L., Johnson D.I., Weith H.L., Somerville R.L.; "Structural analysis of the ileR locus of Escherichia coli K12."; J. Biol. Chem. 261:9966-9971(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94364970; PubMed-8084180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENE MAPPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyrophosphatase of Mscherichia col
J. Bacteriol. 170:5901-5907(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89053923; PubMed=2848015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mapping and disruption of the ches locus in Escherichia coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masuda Y., Ohtsubo E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lahti R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86278038; PubMed=3525538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF 20-116 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pitkaeranta T., Valve E., Ilta I., Kukko-Kalske
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plasmid R100.
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                                                                                                                                                                                                                                                              Query Match
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ĀZĪĒ_BACSU STANDARD; PRT; 157 AA
007920;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JO-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Proline dehydrogenase transcriptional activator.
PUTR OR PF
                                                                             BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cho K., Fuqua C., Martin B.S., Winans S.C.;
"Identification of Agrobacterium tumefaciens genes that direct the complete catabolism of octopine.";
J. Bacteriol. 178:1872-1880(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02452; PemK; 1.
DNA-binding; Complete proteome.
SEQUENCE 116 AA; 12492 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Activator; Plasmid DNA_BIND 29 48 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                SMART:
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39263; AAC43979.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pAtR10.
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                                                                                                                                                                                                                           Local Similarity
nes 7; Conserv
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATORS
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                                                                                                                                                                                      LSKRIGLS 8
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                                                                                                                                                   LSKRVGLS 39
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                                                                                                                                                                                                                                                                                                                                                                          ; PR00033; HTHASNC.
SM00344; HTH_ASNC; 1.
                                                                                                                                                                                                                                                                                                                                                         PS00519;
                                                                                                                                                                                                                                                                                                   156 AA;
                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                         HTH_ASNC_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39, Created)
                                                                                                                                                                                                                                                                                                   17611 MW;
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cumnings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cumnings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.V., Glaser P., Golfeau A., Golightly E.J., Galderon N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl "M. M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl "M. P., Orrestelle D., Formallik S., Prescott A. M.,
Parro V., Pohl "M. P., Orrestelle D., Formallik S., Park S.H.,
Parro V., Pohl "M. P., Orrestelle D., Formallik S., Prescott A. M.,
Parro V., Pohl "M. P., Orrestelle D., Formallik S., Prescott A. M.,
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Parro V., Pohl "M. P., Orrestelle D., Formallik S., Prescott A. M.,
Parro V., Pohl "M. P., Orrestelle D., Formallik S., Parksott A. M.,
Parro V., Pohl "M. P., Orrestelle D., Formallik S., Parksott A. M.,
Parro V., Pohl "M., Port P., Parksott A. M.,
Parro V., Pohl "M., Port
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
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Belitsky B.R., Gustafsson M.C.U.,
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FUNCTION: TRANSCRIPTIONAL REPRESSOR OF
IN BRANCHED-CHAIN AMINO ACID TRANSPORT
SIMILARITY: BELONGS TO THE ASNC FAMILY
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like gene of Bacillus subtills involved in branched-chain
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       Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
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"The com
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Ito K., Kawakami K.,
Submitted (MAY-1992)
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Enterobacter aerogenes.(Aerobacter aerogenes).
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01-FEB-1991 (Rel. 17, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leucine-responsive regulatory protein.
Leucine-responsive regulatory protein.
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MEDLINE-9742661; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
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                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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157 AA;
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                                                                                                                                           Saito N.,
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    EMBL; M35869; AAA24089.1; -. EMBL; D11105; BAA01880.1; -. EMBL; AE000191; AAC73975.1; -. EMBL; AE000796: HAA35614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-E.coli;
SPECIES-92104949; PubMed-1729203;
MEDLINE-92104949; PubMed-1729203;
Oxender D.L., Calvo J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohisubo E., Nakayama K., Murata T., Tanaka M., Tobe J Iida T., Takami H., Honda T., Saskawa C., Ogasawara N., Yasuna, Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli "Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platko J.V., Willins D.A., Calvo J.M.;
"The ilvIH operon of Escherichia coli is positively regulated.";
J. Bacteriol. 172:4563-4570(1990).
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SPECIES-E.coli; STRAIN-0157:H7 / R
MEDLINE-21156231; PubMed-112:8796;
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                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The leucine-responsive regulatory protein: more than a regulator?"; Trends Biochem. Sci. 18:260-263(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D'Ari R., Lin R.T., Newman E.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITINE-94025042; FubMed-8212136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lary S.A., Platko J.V., Oxender D.L., Calvo J.M.;
"Lrp, a leucine-responsive protein, regulates branched-chain acid transport genes in Escherichia coli.";
J. Bacteriol. 174:108-115(1992).
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MEDLINE-90330567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21074935; PubMed-11206551;
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                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                GENES.
SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS, LRP MEDIATES THIS EFFECT FOR AT LEAST SOME OF THESE OPERONS, FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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RESULT 9
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P37424;
01-OCT-1994
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                          microorganisms.";
J. Bacteriol. 177:1624-1626(1995)
-i- FUNCTION: MEDIATES A GLORAL RE
SMART; SM00344; HTH_ASNC; 1.

PROSITE; PS00519; HTH_ASNC_FAMILY; 1.

DNA-binding; Transcription regulation; Activator.

INIT_MET 0 BY SIMILARITY.

DNA_BIND 30 49 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Transcription regulation; Activator; Complete INIT_MET 0 0 H-T-H MOTIF (POTENTIAL).
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                                                                        InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
PRINTS; PR00033; HTHASNC.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-95189743; PubMed-7883720; Friedberg D., Platko J.V., Tyler B., Calvo J.M.; "The amino acid sequence of Lrp is highly conserved in four enteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
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                                                                                                                       EMBL; U02274; AAA75465.1; -.
                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klebsiella
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(Rel. 37, Last annotation
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
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D -> E (IN LRP-1 MUTANT).
B0083495B8F7B255 CRC64;
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LRP_SALTY
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janes B.K., Bender K.A.;

"Two roles for the lendine-responsive regulatory protein in expression of the alanine catabolic operon (dadAB) in Klebsiella aerogenes.";

J. Bacteriol. 181:1054-1058(1999).

-1- FUNCTION: MEDIATES A GLOBAL RESPONSE TO LEUCINE. EXOGENOUS LEUCINE AFFECTS THE EXPRESSION OF A NUMBER OF DIFFERENT OPERONS; LCP MEDIATES THIS EXPRESSION OF A LEAST SOME OF THESE OPERONS. FOR EXAMPLE IT IS REGULATOR OF THE BRANCHED-CHAIN AMINO ACID TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sänderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Kyan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p37403; 087635;
01-OCT-1994 (Rel. 30, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
  EMBL;
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium;
MEDLINE=95189743; PubMed=7883720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of LT2.";
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"The amino acid sequence of Lrp is micrographisms.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                          REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                               GENES
U02273; AAA75467.1; -. AE008741; AAL19894.1; -. AF090144; AAD12584.1; -.
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87.5%;
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    Mismatches

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Pred. No. 8.
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RESULT 15
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ID YGJ3 YEAST
AC P53148;
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DT 01-CCT-1996
DT 01-CCT-1997
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Search completed: January 15, 2003, 11:21:36 Job time: 9.28572 secs
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Best Local (
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53148;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
Hypothetical 104.8 kDa protein in PAN2-NUP145
YGL093W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS: TIGR01177; TIGR01177; 1.

PROSITE; PS01261; UPF0020; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 320 AA; 36673 MW; A879F320AA8CD637 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-97435481; PubMed-9290212; Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.; "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII."; Yeast 13:1077-1090(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01170; UPF0020; 1. Pfam; PF02926; THUMP; 1.
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 917 AA; 104825 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; S0003061; SPC105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z72615; CAA96799.1; -.
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                                                                                                                           594 LAENLNTLKRE 604
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IPR000051; SAM_bind.
IPR0004114; THUMP_dom.
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                             67.3%;
54.5%;
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                                                                                                                                                                                                                                                                          Score 33; DB
Pred. No. 40;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                            8B7ED1522916A319 CRC64;
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                                                                                                                                                                                                                                                                                                           DB 1; Length 917;
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SUMMARIES

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Command line parameters:...

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPT0_spool/US09823649/runat_14012003_151001_29119/app_query.fasta_1.1393
-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX-rng -MINMATCH=0.1 -LOOPELT=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-bloosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -QUTFMT=pto -NORM-ext -HEARSIZE=500 -MINLEN=0 -MAX:EN=2000000000
-USER-US03823649_@CGN_1_1_0_@runat_14012003_151001_29119 -NCPU-5 -TCPU-3
-NO_XLPXY -NO_MADA -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-VGAPOP=10 -YGAPEXI=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - nucleic search, using frame_plus_p2n model
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              January 15, 2003, 11:21:44; Search time 130.143 Seconds (without alignments) 190.345 Million cell updates/sec
                                                                                                           2: SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT: *
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT: *
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                                                          /SIDS2/gcgdata/geneseg/geneseqn-embl/NA2002.DAT:*
                                                                      /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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                               Key
old_sequence
                                                                       Thermosipho africanus
                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                             Mutant thermostable DNA polymerase pTAFI285.
                                                                                                                                                                                                                    AAQ24334 standard; DNA; 1830 BP.
                                                                                                                                                           22-OCT-1992 (first entry)
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  /note= "nucleotides 4-852 deleted from the native
                /*tag=
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AAQ28936
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AAF72306
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ABA21596
AAK00075
AAK25512
AAK110135
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AAV65288
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EST clone H306. H
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

2185239 seqs, 1125999159 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

18: 19: 20: 21: 23:

10: 11: 12: 12: 13: 14: 15: 16:

Scoring table: Sequence: Perfect score:

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US-09-823-649A-6 49

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Xgapop 10.0 , 1 Ygapop 10.0 , 1 Fgapop 6.0 , 1 Delop 6.0 , 1

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US-09-823-649A-6 (1-11) x AAQ24334 (1-1830)
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
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                                                                                                                                                                                                                                                                               1369 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 1401
                                                                                                   Mutant thermostable DNA polymerase pTAFd2-203.
                                                                                                                                                                         AAQ24333;
                                                                                                                                                                                                           AAQ24333 standard; DNA; 2073 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAF1285 causes the polymerase enzyme produced to exhibit a different amt. of 5.7-3.7
                               Thermosipho africanus
                                                                                                                                        22-OCT-1992
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                                                                  5'-3'; exonuclease; PCR;
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90US-0590490.
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                                                                  amplification; SSR; sequencing; PLCR;
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Matches:
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                                                                                                                                                                         AAQ24332
                                                                                                                                                                                        RESULT 3
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                           1612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
         5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2073 BP; 820 A;
                                            Mutant thermostable DNA polymerase pTAF11.
                                                                                   22-OCT-1992
                                                                                                                                                     AAQ24332 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
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90US-0590490
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Mutant thermostable DNA polymerase pTAF09
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2265 BP;
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                                                                                                             AAQ24331 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ23993-Q24013,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in e.g. PCR, sequencing and detection assays
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28-SEP-1990;
28-SEP-1990;
               AAQ28937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced ant. of 5'-3' exonuclease activity may be desirable
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                                                   AAQ28937 standard; DNA; 2568
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2403 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAF09 causes the polymerase enzyme produced to exhibit a different amt. of 5′-3′ exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR23171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abramson RD, Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermosipho africanus
                                                                                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CETU ) CETUS
                                                                                                                                               1 LeuSerLysArgIleGlyLeuSerValScrGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                         also
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ23993 Q24013, AAQ24320-36 and AAQ24343-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0590213.
90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                   947 A;
                                                                                                                                                                                                                                             1.24
49.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "nucleotides 4\text{-}279 deleted from the native sequence."
                                                                                                                                                                                                                                                                                                                                                                                                   257 C; 467 C;
                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                     Matches:
                                                                                                                                                                                                                                                                                                                                                                                                   732 T; 0 other;
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Abramson RD,

28-SEP-1990; 28-SEP-1990; 28-SEP-1990;

30-SEP-1991;

WO9206200-A

old\_sequence

RESULT 4
AAQ24331
ID AAQ2
XX
AC AAQ2
XC AAQ2
XX
DT 22-0
XX
DE Muta

22-0CT-1992

Qy

Percent Similarity:

Alignment Scores:

No.:

Db

1804

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AAQ24330
ID AAQ2
XX
AC AAQ2
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DT 22-(
DT 22-(
DX 5'-:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                        2107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence coding for a thermostable DNA polymerase was isolated from chromosomal DNA of Thermosipho afficanus (Taf). The polymerase (see AAR2312) has 5'-3' exonuclease activity. Deletion of codon 1-37 results in a DNA polymerase which lacks the 5'-3' exonuclease activity. See AAQ23917 for the wild-type Taf Pol I gene and AAQ28936 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Encodes Taf DNA polymerase I lacking 5'-3' exonuclease activity.
                                                     old_sequence
                                                                                                                       5'-3';
                                                                                                                                              Mutant thermostable DNA polymerase pTAFd2-37
                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2568 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 70; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerase from Thermosipho africanus - prepd. by purificn. from cells or by expression of Taf polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR23122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermophilic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostability; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1992
                                                                                            Thermosipho africanus
                                                                                                                                                                             22-OCT-1992
                                                                                                                                                                                                       AAQ24330;
                                                                                                                                                                                                                                 AAQ24330 standard; DNA; 2571 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          another preferred mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                      1 LeuSerLysArgIleGlyLeuSerValSerGlu
                                                                                                                                                                                                                                                                                        CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scores:
                                                                                                                      exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                             (first entry)
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                                                                Location/Qualifiers
                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taf Pol I; deletion mutant;
                            "nucleotides 4-111
            sequence. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
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                                                                                                                                                                                                                                                                                                                                             (1-2568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 494 G;
                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                               Conservative: Mismatches:
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                            deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawyer FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T;
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ID AAQ2
  FIR XXX DEXX
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                                                                                                                                                                                                                                                                        Qγ
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                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                DB:
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              old_sequence
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                                                                                5'-3';
                                                                                                                                                              AAQ24329;
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28-SEP-1990;
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                                                                                                                                    22-OCT-1992
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity alleif discrimination in a combined polymerase ligase chain reaction (PICR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of Thermosipho africanus polymerase DNA which has been mutated. The mutation designated pTAFd2-37 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09206200-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 59; 185pp; English.
                                                                                                    Mutant thermostable DNA polymerase from
                                                                                                                                                                                                  AAQ24329 standard;
                                                                                                                                                                                                                                                               2110 CTTTCAAACAGAATTGGTCTTACTGTTTCAGAG 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2571 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid amplification by PCR, self-sustained sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                          Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ23993-Q24013,
                                                                                                                                                                                                                                                                                            1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1992-150885/18
                                                                       exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR23170
                                                                                                                                    (first entry)
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90US-0590466.
90US-0590490.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1014 A;
                                                                                                                                                                                                                                                                                                                           x AAQ24330 (1-2571)
                                                                                                                                                                                                                                                                                                                                                          49.00
100.00%
100.00%
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                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.35
                                                                       PCR;
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                                                                                                                                                                                                  2679 BP
                                                                       amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ24320~36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 G;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                      Thermosipho africanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŧ;
                                                                     sequencing; PLCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity. See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                 Thermostability; PCR; polymerase chain reaction; thermophilic bacteria; Taf Pol I; mutant; ss.
                                                                                                                                                                                                                                2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2250
                                                                                                  27-OCT-1992
                                                                                                                                   AAQ28936;
                                                                                                                                                                AAQ28936 standard; DNA; 2679 BP
                                                               Encodes Asp37 Taf DNA polymerase I lacking 5'-3' exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2679 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of Thermosipho africanus polymerase DNA which been mutated. The mutation causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable DNA polymerases with altered 5'-3' exo nuclease
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                                                                                                                                                                                                                                                 1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RD,
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1045 A; 295 C; 515 G; 824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  1.42
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                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
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RESULT 9
AAQ23917
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W09206202-A
                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence coding for a thermostable DNA polymerase was isolated from chromosomal DNA of Thermosipho africanus (Taf). The polymerase (see AAR23122) has 5'-3' exonuclease activity. Mutation of the codon specifying cly at position 37 (i.e. GGA) to an Asp codon results in a DNA polymerase which lacks the 5'-3' exonuclease activity. See AAQ23917 for the wild-type Taf Pol I gene and AAQ28937 for another
                                                                                                              Thermosipho africanus
                                                                                                                                        Thermostability; PCR; polymerase chain reaction; thermophilic bacteria; Taf Pol I; ss.
                                                                                                                                                                                        Taf DNA polymerase I coding sequence.
                                                                                                                                                                                                                           27-OCT-1992 (first entry)
                                                                                                                                                                                                                                                             AAQ23917;
                                                                                                                                                                                                                                                                                              AAQ23917 standard; DNA; 4286
                                                                                                                                                                                                                                                                                                                                                           2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2679 BP; 1045 A; 295 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 70; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerase from Thermosipho africanus - prepd
by purificn. from cells or by expression of Taf polymerase gen
in host cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preferred mutant.
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                         /product= Polymerase_1
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298..2976
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/note= "Gly codon changed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified with degenerate primers corresponding to the amino acid sequences of conserved regions of known thermostable polymerases. When specific PCR products of a similar size to the product generated using Tag chromosomal DNA were produced, the PCR fragments were cloned and sequenced. Fragments with sequences which encoded regions of amino acid homology to known thermostable polymerases were identified. The cloned PCR products were used as probes to screen a genomic Southern blot. The full-length Taf coding sequence was then compiled from various clones. See also AAQ23918-Q23961.
                                                                                                                                                                                                                          Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2515
                                                                                                                                                                                                                                                            megabase shotgun sequencing method; open reading frame; ORF;
                                                                                                                                                                                                                                                                                                                                                        27-MAR-1997
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                                                                                                                                                                                                                                                                                                                  Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 6; 80pp; English
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                                                                                                                                                                                                                                                                               genitalium; DNAA; DNA gyrase; origin of replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG
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                                                         "Previously identified as MORF-20076, the encoded protein shows 27.59 percentage identity to thymidylate kinase (CDC8) from Saccharomyces cerevisiae"
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                                                                                                                                  MG006
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                            from B.
40543.41787
/*tag= l
                                                                                                                                                                  identity to glycerol uptake facilitator (glpF) from B. subtilis" complement (39873..40514)
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                                                                                                                                                                                                                                                                                                                             "Previously identified as MORF-20099, the encoded protein shows 26.82 percentage identity to ATP-dependent nuclease (addA) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Previously identified as MORF-19826 and MORF-20093, the encoded protein shows 46.84 percentage identity to GTP-binding protein from E. coli"
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                                                                    "Previously identified as MORF-20101, the encoded protein shows 48.13 percentage identity to thymidylate kinase (tdk) from B. subtilis"
"Previously identified as MORF-20102, the
                                                                                                                                                                                                                                   "Previously identified as encoded protein shows 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Previously identified as MORF-20092, the encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (tsr) from B. subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Previously identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded protein shows 25.73 percentage identity to DNA primase (dnaE) from Clostridium acetobutylicum"
                      MG035
                                                                                                                                                 MG034
                                                                                                                                                                                                                                                                           MG033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded protein shows 32.23 percentage identity to transport ATP-binding protein (msb) from E. coli"
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51525__52382
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identity to phosphohistidinoprotein-hexose
phosphotransferase (ptsH) from Mycoplasma
                                                     phosphorylase (deoD) from E, coli<sup>n</sup>
59083..59754
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52366..53220
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                                                                                                                                                                                                                                                                                        "previously identified as MORF-20112, the encoded protein shows 36.60 percentage identity to sialoglycoprotease (gcp) from Pasteurella haemolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Previously identified as MORP-19832 and MORP-20108, the encoded protein shows 41 percentage identity to spermidine/ putrescine transport ATP-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Previously identified as MORF-20105, the encoded protein shows 46.83 percentage identity to glycerol kinase (glpK) from E. coli"
                                                                                                              "Previously identified as MORF-20114 and
                                                                                                                                                                                   "Previously identified as MORP-19834, MORF-20114 and MORF-20115, the encoded protein shows 43.02 percentage identity to signal recognition particle protein (ffh) from B.
                                                                                                                                                                                                                                                                                                                                                                                                                     *Previously identified as MORF-20111, the encoded protein shows 29.45 percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "previously identified as MORP-20110, the encoded protein shows 26.51 percentage identity to spermidine/putrescine transport system permease protein (potB) from E. coli
"Previously identified as MORF-20117, the encoded protein shows 83.03 percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Previously identified as MORF-19831 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MG038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
мс043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORF-20106, the encoded protein shows 43.20 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded protein shows 30.71 percentage
identity to histidyl-tRNA synthetase (hiss)
from Mycobacterium leprae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MG044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MG042
                              MG050
                                                                                 MORF-20115, the encoded protein shows 44 percentage identity to purine-nucleoside
                                                                                                                                                                          subtilis"
                                                                                                                                                                                                                                                 MG048
                                                                                                                                                                                                                                                                                                                                                    MG046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capricolum"
                                                                                                                                                                                                                                                                                                                                                                                                          identity
                                                                                                                                                                                                                                                                                                                                                                                          ty to spermidine/putrescine transport permease protein C (potC) from E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from E. coli"
                                                                                                  44.78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli"
                                                                                                                                                                                                                                                                                                                                                              AAF22306/c
ID AAF223
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
 Db 416013 CTGAGTAAACGGTTAGGATTATCAGTTAGT 416042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-823-649A-6 (1-11) x AAT58840 (1-580073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment
                                                                                                                                                                                                                                                                                                                       XX AC XX
                                                                     18-MAR-1999;
01-APR-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                    AAF22306;
                                                                                                                                                                                                                                                                                                                                                                 AAF22306 standard; DNA; 163319
               (UYCH-) UNIV CHICAGO
                                            13-SEP-1999;
17-SEP-1999;
                                                                                                                               17-MAR-2000;
                                                                                                                                                            21-SEP-2000
                                                                                                                                                                                       WO200055325-A2
                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                               Centromere;
                                                                                                                                                                                                                                                                            Arabidopsis thaliana chromosome 4 centromere.
                                                                                                                                                                                                                                                                                                         20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LeuSerLysArgIleGlyLeuSerValSer 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scores:
                                                                                                                                                                                                                                               michrosome;
                                                                                                                              2000WO-US07392
                                                                                                                                                                                                                                                                                                        (first entry)
                                        99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                  99US-0125219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identity to deoxyribose-phosphate aldolase (deoC) from Mycoplasma pneumoniae" complement (64898..65731)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SPase)
91065..91919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81047..82597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (65713..66249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= MG057
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42.00
100.00%
90.00%
85.71%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Previously identified as MORF-20136, the encoded protein shows 34.8 percentage identity to ribosomal protein S2 (rpS2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Previously identified as MORF-19845, the encoded protein shows 28.84 percentage identity to glutamic acid specific protease (SPase) from Staphylococcus aureus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Previously identified as MORF-20123, the encoded protein shows 38.90 percentage identity to the protein disclosed in GB:D26185_104 from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Previously identified as MORF-20122,
encoded protein shows 30.25 percent
identity to the protein disclosed in
GB:D26185_99 from B. subtilis"
                                                                                                                                                                                                                                               vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MG070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MG067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spirulina plantensis"
                                                                                                                                                                                                                                                                                                                                                                 ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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Indels:
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Conservative:
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**ភ្លាក្រុងស្ត្រាក្នុងស្ត្រាក្នុងស្ត្រាក្នុងស្ត្រាក្រុងស្ត្រាក្រុងស្ត្រាក្រុងស្ត្រីក្រុងស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្តិត្រីស្ត្** 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43646 CTTTCAAAACGAATTGGCGTGTCCGTGTCA 43617
                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
            The invention
                                                 Claim 1; SEQ ID NO 72; 639pp + sequence listing; English
                                                                                        analyzıng
                                                                                                               Human
                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                    27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002
                                                                                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                  03-AUG
                                                                                                                                                                                                                                                                                                                                                   30-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selected proteins such as hormones, enzymes, interl factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f} the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA51767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA51767 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 163319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587529/55
                                                                                                                                                                                                                                                                                                           21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuSerLysArgIleGlyLeuSerValSer 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to a recombinant DNA construct of a plant
                                                                                                                                                                                          SG,
                                                                                                                                                  2001-483447/52
                                                                                      genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetal liver single exon nucleic acid probe #72.
                                                                                                                                                                                                                                                                                                                                                   -2000;
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                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 1389-1451; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copenhaver
                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-02324687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        liver;
            relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 53475 A; 30117 C;
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90.00%
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41.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression; single exon nucleic acid probe;
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          to a single exon nucleic acid probe for
                                                                                                                                                                                        Chen W,
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                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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Mismatches:
Indels:
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          Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment
                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                       Penn
                                                                                                                          The present
                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 471
                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA21596;
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                                                                                                                                                                                                                         exon
                                                                                                                                                               SEQ ID
                                                                                                                     invention relates to single exon nucleic acid probes for
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                   WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA21596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TTAACAAAACGGGTAGGCTCTTCAGTTTCAGAG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuSerbysArgIleGlyLeuSerValSerGlu 11
                                                                                              MOLECULAR DYNAMICS
                                                               Hanzel DK,
    nucleic
                                                                                                                          ; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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                                                                                                                                                                                                        2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                          2000US-0608408
                                                                                                                                                                                                                         2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression analysis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 471
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acid probes
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                                                               Rank DR;
for analyzing gene expression
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Query Match:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          Single
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   Sequence 471 BP; 117 A; 94 C; 104 G; 156 T; 0 other;
                                                           epilepsy and
                                                                                                                                                The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                    Example 4; SEQ ID NO: 66; 650pp + Sequence Listing; English.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                  SG,
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                                                                                                                                                                                                                                                                              2001-483446/52
                                                                                                                                                                                                                                        exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
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2000US-0334687.
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                                                           The present sequence
                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-471)
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Best Local Similarity:
US-09-823-649A-6 (1-11) x AAK25512 (1-471)
                                                         Query Match:
                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                            Score:
                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                       bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer
                                                                                                                                 No.:
                                                                                                                                                                                  Sequence 471
                                                                                                                                                                                                                       the probes
                                                                                                                                                                                                                                          such as lymphoma,
                                                                                                                                                                                                                                                                                             probes which are derived from
                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 69; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                     analyzing
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful
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2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                 117 A; 94
                                                                                                                                                                                                                       invention
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Search completed: January 15, 2003, 12:56:51 Job time: 202.143 secs

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US-09-199-637A-26/c
; Sequence 26, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 CTTTCCAAACGATGCGGTCTGAATCTTTCT 238
                                                                                                           485 AGTAAAAGGATTGGGTTAAGCCGTTCT 459
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                                                                                                                              2 SerLysArgIleGlyLeuSerValSer 10
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FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfe CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blattner, Frederick R.
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Bec-1999 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 635
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Matches:
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Best Local Similarity:
Query Match:
Search completed: January 15, 2003, 12:58:54 Job time : 31 secs
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                                                                                                                                         US-09-823-649A-6 (1-11) x US-09-199-637A-26 (1-642)
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                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 26
LENGTH: 642
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
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APPLICANT:
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                       371 TTAGCCAAGCGGTTTGGCCTCTCGGTC 345
                                                                                         1 LeuSerLysArgIleGlyLeuSerVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
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Cao, Hui
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33.00
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Crossland, Lyle D

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US-09-823-649A-6 (1-11) x US-09-575-602-11 (1-6596)
                                                              Best Local Similarity:
                                                                                               Score:
                                                                                                                                                               US-09-575-602-11
                                                                              Percent Similarity:
                                                                                                                             Alignment Scores:
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INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             FEATURE:
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OTHER INFORMATION: /fur
OTHER INFORMATION: B200
OTHER INFORMATION: /evi
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                NO. . .
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LOCATION:
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REFERENCE/DOCKET NUMBER: CGC 1915/Reg
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                                                                                                                                                                                                                                                                                                         /function= "3' Regulato
for B200i4-2"
/evidence= EXPERIMENTAL
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                                                                                                                                                                              /function=
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B20014-2"
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                                                                                                                                                                             "translation stop"
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                                                                                             Hatches:
                                             Mismatches:
Indels:
                                                                            Conservative:
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RESULT 13
US-09-221-017B-720/c
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                                Percent Similarity:
Best Local Similarity:
                                                                                Pred. No.:
                                                                                             Alignment Scores:
                                                                                                                              US-09-221-017B-720
                  Query Match:
                                                                Score:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ROSS, BRUCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1175
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APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE: 1
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APPLICATION NUMBER: 1
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FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monroy, Gladys REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PP11 FILING DATE: 31-DEC-1997
                                                                                                                                            LOCATION:
                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                       TOPOLOGY:
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5. 6444799
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Gaps:
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US-08-961-527-181
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                              US-09-823-649A-6 (1-11) x US-08-961-527-181 (1-8651)
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Query Match:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    TELEPHONE: (301) 309-851
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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|||:::|||:::||||||::::|||
2152 TCCAGAAGACTTGGCCTATCTAACGAA 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                            No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doub
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REFERENCE/DOCKET NUMBER: PB340P1
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1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
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                                                                                                                                                                                                                                                       LENGTH: 8651 base pairs
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                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                    Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maryland
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                                                                                                                                                                                                                                                                                                                     (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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Indels:
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RESULT 12
US-09-575-602-11
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                                                                                                                                                               US-09-823-649A-6 (1-11) x US-08-905-223-39 (1-427)
                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                    US-08-905-223-39
                                                                                                                                                                                                                                                 Percent Similarity:
Sequence 11, Application US/09575602 Patent No. 6392123 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08905223 Patent No. 6222029
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israclsen, Ned A.
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LACTOIX, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 427 base pairs
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                                                                                                                                                                                                                                                                                  NO . .
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                              332 TTGGCAAAGACCCTGGGACTCGAGGTGAGTGAG 364
                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: Von Heijne matrix OTHER INFORMATION: score 10.8 OTHER INFORMATION: seg VLLFFVLLGMSQA/GS
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide
LOCATION: 191..268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapiens
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                                                                                                                              1 LeuSerLysArgIleGlyLeuSerValSerGlu 11
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US-09-823-649A-6 (1-11) x US-08-987-151-3 (1-1785)
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Patent No. 6255070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Willison, Keith Robert
APPLICANT: Kubota, Hiroshi
APPLICANT: Ashworth, Alan
TITLE OF INVENTION: Folding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1785 base pairs
                                                                                        SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1065 UCCAGAAGACUUGGCCUAUCUAUUAACGAA 1094
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                STREET: Two Emparcas
CITY: San Francisco
                                                 APPLICATION NUMBER: US/08/687,590 FILING DATE: 31-JUL-1996
                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,
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COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                   CLASSIFICATION:
                                                                                                                                                                                                          COUNTRY: United States of America
                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                   ADDRESSEE:
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Lilly Corporate Center
                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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                                                                                                            PatentIn Release #1.0, Version #1.25 (EPO)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 16
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REFERENCE/DOCKET NUMBER: 0:
INFORMATION FOR SEQ ID NO: 61:
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ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
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LOCATION:
                                                                         REFERENCE/DOCKET NUMBER:
                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                         FILING DATE
                                                                                                                                                                                     CLASSIFICATION: 424
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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:: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                            9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                             Diskette, 3.50 inch, 1.4Mb storage
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Indels:
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RESULT 6
US-08-987-151-1
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Best Local Similarity:
Query Match:
; Sequence 1, Application US/08987151
; Patent No. 6162617
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                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
US-08-987-151-4
                                                                                                                                                               US-09-823-649A-6 (1-11) x US-08-987-151-4 (1-1602)
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                                                                                        1158 TCCAGAAGACTTGGCCTATCTATTAACGAA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burgett, Stanley G.
APPLICANT: Rosteck Jr., Paul R.
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE :,F INVENTION: dnaG
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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APPLICANT: Peery, Robert B.
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STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                         2 SerLysArgIleGlyLeuSerValSerGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/987,151
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Indels:
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Best Local Similarity:
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US-08-987-151-1
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                                                                                                                                                           Sequence 3, Application US/08987151 Patent No. 6162617
                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Jaskun
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                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                              1065 TCCAGAAGACTTGGCCTATCTAFTAACGAA 1094
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CORRESPONDENCE ADDRESS:
                           APPLICANT: Rosteck Jr., Paul R.
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: dnag
                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
FEATURE:
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LENGTH: 1785 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
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                 NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: X-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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                                                                             Burgett, Stanley G.
                                                                                           Peery, Robert
                                                                                                              Zhao, Genshi
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36.00
100.00%
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                                                                                                                              Stanley R.
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US 609,157

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Case No. 2580

US 455,611

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; LOCATION:
US-08-458-819-11
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PCT-US91-07035-11
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Query Match:
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APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2250
                            PRIOR APPLICATION DATA:
                                                                                    PRIOR APPLICATION DATA:
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 7.
FILING DATE: 15-AUG-1991
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 59
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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                                           APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 22-AUG
                                                                                                                                                                                                                           FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                       FILING DATE: 12-JAN-1988
                                                                                                                                                                                                                                                                                                                                                 FIL:NG DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: POFILING DATE: 19910930
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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      APPLICATION NUMBER: US 585,471
                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 143,441
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Indels:
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Best Local Similarity:
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                                                                                  Alignment Scores:
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                                                                Pred. No.:
                                                                                                                        ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2379
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                                                                                                                                                                                            PRIOR FILING DATE: 1997-11-08
PRIOR FAPELCATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6380370
                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCCEIC ACID AND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: BPIDERHIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT FILLOGATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTCAGAG 2250
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MOLECULE TYPE:
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LOCATION:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Gaps: Indels: Mismatches: Conservative: Matches: Length:

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Conservative: Mismatches: Matches:

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Best Local Similarity:
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                                                                                                              US-08-458-819-11
                                                           Sequence 11, Application US/08458819
Patent No. 5795762
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11
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                                                                                                                                                            2218 CTTTCAAAGAGAATTGGTCTTAGTGTTTTCAGAG 2250
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APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LENGTH: 2679 base pair:
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APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
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APPLICATION NUMBER:
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LOCATION:
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TELEPHONE: (510) 814-2972 INFORMATION FOR SEQ ID NO: 11:
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FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
PRIOR TOATTON NUMBER: US 063,509
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: Ca
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 58
FILING DATE: 20-SEP-1990
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 557,517 FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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            HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2679 base pair
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ORIGINAL SOURCE:
                                                MOLECULE TYPE:
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                                                                  TOPOLOGY:
                                                                             STRANDEDNESS: single
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                                              DNA (genomic)
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Minimum DB
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  of hits satisfying chosen parameters:
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US-08-987-151-3

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US-08-967-150-61

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                COMPUTER: Macintosh OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                       PRIOR APPLICATION DATA:
                                                    APPLICATION NUMBER: FILING DATE: 28-SEP
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                     APPLICATION NUMBER: FILING DATE: 28-SEP
                                                                                                                   CLASSIFICATION: 435
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US-08-755-587-28
US-09-19-637A-22
US-08-557-128-2
US-09-19-637A-12
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US-09-19-637A-12
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Sequence 71, Appli
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Sequence 76, Appli
Sequence 25, Appli
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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ALIGNMENTS

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Sequence 11 from patent US 5795762.
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Matches:
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Indels:
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                                             DNA
f 51
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser,C.M., Gocayne,J.D., White,O., Adams,M.D., Clayton,R.A., Fleischmann,R.D., Bult,C.J., Kerlavage,A.R., Sutton,G.G., Kelley,J.M., Fritchman,J.E., Weidman,J.F., Small,K.V., Sandusky,M., Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Saudek,D.M., Phillips,C.A., Merrick,J.M., Tomb,J., Dougherty,B.A., Bott,K.F., Hu,P.C., Lucier,T.S., Peterson,S.N., Smith,H.O. and Venter,J.C. The minimal gene complement of Mycoplasma genitalium Science 270 (5235), 397-403 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann, R.D., Bult, C.J., Kerlavage, A.R., Sutton, G.G., Kelley, J.M., Fritchman, J.L., Weldman, J.F., Small, K.V., Sandusky, M., Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Saudakl, D.M., Phillips, C.A., Merrick, J.M., Tomb, J.-F., Dougherty, B.A., Bott, K.F., Hu, P.C., Lucier, T.S., Peterson, S.N., Smith, H.O. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-OCT-1995) The Institute for Genomic Research, Medical Center Drive, Rockville, MD 20850, USA (bases 1 to 12486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr, Rockville, MD 20850, USA
On Nov 5, 1998 this sequence version replaced gi:1046022.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-OCT-1998) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser, C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma 1 (bases 1 to 12486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma genitalium
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                                                                                                                                                                                                                                                                                                                           /codon_start-1
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/protein_id="AAC71550.1"
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                                                                                                                                                                           complement(914. .1720)
/gene="MG327"
                                                                                                                   identity: 66.17; identified putative"
                                                                                                                                                                                                                                                                         QLAKELSEQNKDKEFLVFETSDIA ISLKWLVEDIKALVDKGCDNOTIKAKVESHKQNI
LSAVTLKNLVQMRKGGRISGLKKFITTLLRVKPIILFDKGVNTLGAKVFSFSQAVEKI
FGFVKTKFGDNYKIKRIGFCYSFCKNYANBIKKIITDFIBHNKINFQNBIENAFITSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(14. .901)
/gene="MG326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(14. .901)
/gene="MG326"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:U00089
identity: 68.94; identified
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                       /transl_table=4
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/db_xref="GI:3844907"
                                                                                                                                     /note="similar to GB:U00089 SP:P75311 PID:1674047 percent
identity: 66.17; identified by sequence similarity;
                                                                                                                                                                                                                     /gene="MG327"
                                                                                                                                                                                                                                       complement(914. .1720)
                                                                                                                                                                                                                                                         IIVHTGIDAFSISLLIDNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:2097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mycoplasma
                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'isolate="G37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genitalium"
                                                           putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP:P75312 PID:1674048 percent by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712
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gene

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complement(1707. .3977)
/gene="MG328"
complement(1707. .3977)
/gene="MG328"
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putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MG329"
complement(4016. .5362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NELKKLHDNTSNDENEKYDDLLNQYELLFDENETKFDKLQVKQQALNLDYQKTISALK
HENDYLLDE IEWTRSKDNDFNNYKNSFEEQKKALDEKINGLTIQNQQLQDKIAELSEE
NENNILLAKLQADHEILQESYGKLKTDFEKLKKKKLNDANEOYQDLLSAFEETNISELEK
AKQSLSASDSENNQLKQQINSLENAKKELQFTPYTSDEHLDELETLKIEKGLFLENQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
/protein_id="AAC71552.1"
/db_xref="GI:3844908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKKKKWPFFTTNFPGHGDNESTDTDQLKLNHFVDLVCDFIVQKKLNNVILIGHSMGGA
VAVLVNKVIPLKIKALILVAPMNQTSFSVNKKRILDTFFKRNNSNHKDFVEHEEKRKS
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                         /note="similar to GB:U00089 SP:P75307 PID:1674042 percent
identity: 39.34; identified by sequence similarity;
putative"
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QVNELNIDLFLKIINQIWWFFEKDAVYYNNADITFVITTQSVANIASKIAVDPNIRKI
AVIKQQKLAENKNIYWDGBDIGTVYLKNAQLKFFLDAKVEIRAQRRLDDWGISLSNEK
KLKELIQELKQRDQIDSSRTADPLKKAQDAIYLDTSELSFDAVVKQTLKEAKKVFKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5366. .6019)
/gene="MG330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPLKVNGEKFLLIDTAGIKRKGKINMGIETASYIKTKLAIARSNVILLMVDGSKPISE
QDEVIGGLAQAALIPVIILYNKWDLVLKNNNTTNAYKKMLKLHFKHLDFAPVLFISVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EWLKRK IAF I DTGGL I AKQTPLQQL I ALQVQAAL SQAKA I I FLVSLQEQL NSDDFYVA
KVLKKNKDKPV I LVVNKAENENPKTAEETLKDYY SLGFGRPVV I SAAHG I G I GDLMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRRLSEEKSKHLHTKKLQDDLLQENRDLYEQLQNKPVAINPLSDEVNEELENLKQEKA
LLSDQLDALKNKSSNVQQQLALLPVLNNQINELQNQLLTAREANQRLDLVEQENDFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVKRILKEQHPTKKVDELDDYNNKELLLENADLKKQIDDLKENNNDQIFDLEQEIDDL
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QPSEEINETKKPEVQIFSTDKVKEPEQFDDFYSIENLIKAINPVHKTIQYDQNDDQPF
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                                                                                                                                                    complement(6028. .6666)
                                                                                                                                                                                                          complement(6028. .6666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5366. .6019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQIPHFVLFCNDPKYLHESYARFLENKIRENFGFNSVPISLYFKSKNARIRTKPEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNQRLNTIFEQLKIIQSQLETKVATPLLNDVIQQAQUYNQPPLFKGKRLQITYAVQTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:U00021 PID:467147 percent identity:
32.18; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4016. .5362)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERNILEKTFFGTVDEAEKEKSIVSFFNWMIDLKVLDKKWDKNVLNHYANQLKTREEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MAVDKELEISDFDNELDEKTLLKELVQRTNNILFSPSKITAIPF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=4
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identity: 65.42; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MG330"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MFTVAIIGRTNVGKSTLFNRLIQKPMAIVSDTPNTTRDRIFGIG/
                                                                                                                                                                             /gene="MG331"
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   VERSION
KEYWORDS
                                                                                                                                                                             RESULT 4
AC124922/c
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                                                                                                                                                                                                                                                                                                                                  γQ
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                                                             ACCESSION
                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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HTG; HTGS_PHASE1
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gene CDS

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US-09-823-649A-6 (1-11) x U39714 (1-12486)
                                                                                                                                                                                                         7057 CTGAGTAAACGGTTAGGATTATCAGTTAGT 7086
                                                                                                                                                                                                                                       1 LeuSerLysArgIleGlyLeuSerValSer 10
                        AC124922
                                                                         Rattus norvegicus clone CH230-397L24,
AC124922.2 GI:21671429
                                                                                                    AC124922
                                                 28 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:U00089 SP:P75306 PID:1674041 percent identity: 75.64; identified by sequence similarity; putative"
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QKYEDADDDKSEWIMWALNQSEIIKROLKSIGVCLMWSEYKFILSEQANKIVNNCF
KNLZENGFIYQAYTLVNWDTKLUTALSINIEVINKEYNOHLHYVVYKLANDSKQELIVA
TTRPETIFADVCLLVNPKDKRYTNEWNKLVVNPLTGKQIPVYTDSYVDIKFGTGILKC
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/trans1_table=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identity: 63.96;
putative"
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/gene="MG334"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is not the result of a sequencing artifact; similar to GB:000089 SP:P75305 PID:1674040 percent identity: 74.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7380. .7974)
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HLKVAVDLALAKGLSMDSIKRNIHGSEKDTIKISEFCYEIFGPNGVGIIVFGLTDNPN
RLLSSLNGYLAKLKGQLAKPNSVKINE;;5.5GIIFVNKNNYLKDDLIELLILDNINLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
/protein_id="AAC71556.1"
/db_xref="G1:3844912"
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complement(6654..7373)
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/protein_id="AAC71555.1"
/db_xref="g1:884911.1"
/translation="MGRYEKFRFYRQSFDNNKIVKKALINAQKNTESWKKQLNKINQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPAHDENDYEI NTKYKFUFLSCIDSNGILNQNASKFQGLSVI,QARNKIVKWLEKNKLL
VKSIPLTSNVGFSERSGTVVEPMLSKQWFVDLPKLKDHLYLKKYPDFIPKRFNKQVSN
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                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hullyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maksey,E., Mawhiney,E., McLeod,M.P., Meaton,M., Mei,G., Metcker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,B., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Wallams,G., Williams,G., Warren,R., Washington,C., Watlington,S.,
Whi,Y.F., Warren,R., Washington,C., Watlington,S.,
Whi,Y.F., Zhon,J., Zorrilla,S., Nelson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Brya
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chaves
                                                                                                                                                                                                                                       Baylor
On Jul
                                                                                                                                                                                                                                                                                                                                                 Submitted (20-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 147168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, G., Chen, R., Chan, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                     Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria;
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Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bc
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Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                 Jul 2, 2002 this sequence version replaced gi:21490014.
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  Center project name: GYQQ
Center clone name: CH230-397L24
Center clone name: CH230-397L24
Chemistry: Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                              Center code: BCM
                                                                                                                                                            Web site:
                                                                                                                                                                                             Center: Baylor College of Medicine
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                                                                                                                                                        http://www.hgsc.bcm.tmc.edu/
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                                                            FEATURES
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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147168: contig of 17092
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6: contig of 12599 bp in length
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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                            consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
TE: This is a 'working draft' sequence. It currently
                                                                                 it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (05-FEB-1997) Biology, Indiana University, Bloomington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \label{eq:continuous} Ferkowicz, M.J., \quad Stander, M.C. \quad and \quad Raff, R.A. \\ Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad of \quad three \quad Phylogenetic relationships \quad and \quad developmental \quad expression \quad developmental \quad development
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Ferkowicz,M.J., Stander,M.C. and Raff,R.A.
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a 29771 c 29664 g 38958 t
                                                                                                                                                                                                                                                                                                                                                                                          /product="Wnt-4 protein"
/protein_id="AAC69242.1"
/protein_id="AAC69242.1"
/protein_id="AAC69242.1"
/db_xref="G1:11857936"
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/translation="GHYLDNGTBEAAFVNA1SAAGVANAVFRGCGSGELEKCGGDRTV
/translation="GHYLDNGTBEAAFVNA1SAAGVANAVFRGCSGSGELEKCGGDRTV
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/GNSAEGFWAAGCSGENTCWKSAATAGCGSAGFNT
NADFKPHTSSDLVYLVPSPDFCEEDLKGSLGTHGRRCNKTSKAIDGCELMCCGRGFNT
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cysteine residues"
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/note="secreted glycoprotein with several con
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10673 bp DNA linear BCT 28-JAN-199 Methanococcus jannaschii section 88 of 150 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-AUG-1996) The Institute for Genomic Research, 9712 Medical Center Dr. Bockville, MD 20850, USA on oct 3, 1996 this sequence version replaced 91:1564062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kelley, J.M.,
Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A.,
Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii Science 273 (5278), 1058-1073 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kellcy, J.M., Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A., Peterson, J.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.
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Bult, C.J., White, O.,
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Archaea; Euryarchae
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Euryarchaeota; Methanococci; Methanococcales;
                                                                  DVGRVFPISASISIFILIGLIYSLSSINKTSSTLTEFIGEFILHFVDSITLSILLIA
VGRFVDTIINSEKDILELLKKYFFCLICIFISRELIISGGEVILKKISFIMFVMCVII
                                                                                                                                                                      /translation="mekegyknylvlyvdIdDDIGRKAGLNTPILGREENIKALIKLG
LADPGDSDYNAILGGYKIYDELKASGKDVEIATISGDVDVESEKCALRIKEQIDFLLY
LYNPDFIYLVSDGKEDEMILKYLESKNIFVNKKRVIVKQSETLESTYYLLGEFIKKIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Methanocaldococcus jannaschii"
/db_xref-"taxon:2190"
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                                     YISIVIILSVILFTKSSKEDKFKKLKNSITKG"
                                                                                                                                                SEYTPL1LTF1GFSL1LYATFAD1GWR1VVG11GLY1LSEGVGVRKLLMEK1KKKEEF
                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAB99036.1"
/db_xref="GI:1499875"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GB:AE000782 percent identity: 34.62;
identified by sequence similarity; putative"
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/transl\_table=11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MJI034"
/note="similar to GB:X12791 SP:P09132 PID:36113 percent identity: 32.89; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYYDTLQLIDMSATYREVLTSMMDITLSLENIKMNQIMKILTMYTTIFAVPMWITGI
YGMNESYLPLANNEQGEWLYMALMYVIIMIEVYIFRRSGWI"
2154. 2417
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/note="similar to GB:L42023 SP:P44998 PID:1006270
PID:1205285 PID:1221151 percent identity: 25.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to PID:685181 PID:726050
GB:AE000666 percent identity: 66.43; ide
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="MJ1034"
2154. .2417
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TIHSDKIKAIGRLHKLISTKKPRIVFERGIGFLLYHILNEITRSYSRILMNLEDELEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MJ1036"
3682. 4383
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E″
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/gene=#MJ1035"
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PKIYRDKRYPRQHWEICGCYEVDYKGNKLQLLKEICKIIKGKN"
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/protein_id="AAB99037.1"
/db_xref="G::1499876"
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1191. .2144
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IDAVKEGKEIELPKIVITEQKAVEAMEFTNPYAKAKAMAAFTIAEKVGDVDVKGCFMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="signal recognition particle,
/protein_id="AAB99038.1"
/db_xref="GI:1499877"
/note="similar to PID:1054861 SP:P50909 percent identity:
64.12; identified by sequence similarity; putative"
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                                                                                                                                                                               YILLGYILVGIIALH"
                                                                                                                                                                                                        KFIYPISFFIHTFIDGLIIAVSYISEIGLPLYLAILMHKLPAGFVLISPLKGVYKNPL
YPGVFVSFGTVLGTIVGLVTLKDVSTKILLAFSGGVFLGAFLMLAPHIYEHKEEKTFL
                                                                                                                                                                                                                                                           /translation="mSNMVEVPIFIAILSFIVMCIGELLAYYSVSLKYKYEFEAISFG
FIFGVATLILIPKSYSNMFVLYVILGMITVYLIEKYLAYCPLSKKYCVECDNLEENRI
                                                                                                                                                                                                                                                                                                            /product="M. jannaschii predicted coding region MJ1036"
/protein_id="AAB99045.1"
/db_xref="GI:1591689"
                                                                                                                                                                                                                                                                                                                                                                                                                                              putative
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/note="hypothet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MJ1035"
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                                                                      'gene="MJ1037"
                                                                                                                               'gene="MJ1037"
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                                                                                                         .5660
                                                                                                                                                          5660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ypothetical protein; identified by GeneMark;
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entified by
                                                                                                      Alignment Scores:
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/gene="MJ1038"
5837. .6691
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6866...710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //note-"similar to GB:X73293 PID:505290 SP:P41558 percent identity: 70.99; identified by sequence similarity: putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MJ1039"
6866. .7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:M65060 SP:P26920 PID:149750
GB:AE000666 percent identity: 47.77; identified i
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MKVTDHILVPKHEIVPKEEVEEILKRYNIKIQQLPKIYEDDPVI
QEIGAKEGDVVRVIRKSPTAGVSIAYRLVIKRII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity; putative"
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LGQALLAKKMGKKRVIAETGAGQHGVATAAACAKLGLECIIYMGAKDVERQKLNVERM
ELMGAKVIPVEGGSQTLKDAVNEALRDWTTNVRTTYYLLGSALGPHPYPMAVREFQRV
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QIPLVILMKALGAETDKDIIESIDDERFFMEIVLNIQEIREEHNINSPEDALEFIGKR
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/protein_id="AaB89042.1"
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PID:809732 percent identity: 49.33; identified b
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TPDERLKKILEKCSGFVYVVSVTGITGAREKVAEETKELIKRVKKFSKIPACVGFGIS
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AX059549
          Submitted (30-APR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, MO 63108, USA 4 (bases 1 to 63292)
                                                                                                                                                                                          Arabhidosis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 63292)
Harmon,G., Wohldmann,P. and Lehnert,L.
The sequence of A. thaliana F14G16
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Location/Qualifiers
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                                                              Direct Submission
                                                                               Waterston, R
                                                                                                                               The A. thaliana Genome
                                                                                                                                           2 (bases 1 to 63292)
Washington University
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 Waterston, R.
                                                                                                          Unpublished
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                                                                                                                  Submitted by:
                                                                                                                                       Submitted (13-AUG-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, MO 6~108,
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                              Waterston, R.
Department of Genetics, Washington University, St. Louis, MO 63108, USA e-mail: rwilson@watson.wustl.edu
                                                                                    Genome Sequencing Center
                                                                                                                                                USA
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M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing. MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone This sequence was finished as follows unless otherwise noted: neighboring submissions. NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between

## NEIGHBORING COSMID INFORMATION:

The 3' clone is F28D6, 200 bp overlap. Actual is at base position 1 of F14G16; actual end is start of this clone at 41649 of F28D6

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation) Location/Qualifiers

Green and L. Hillier, ms in preparation).

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1528. .1684 /note="F14G16"

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Allen,C., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Danks,T., Barboraks,S.L., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Benton,J., Binage,K., Blankenburg,K., Bynnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Clen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Dalgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flaggy,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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21183 . 22195.
/gene="F14G16.2"
/join(21183 . 21320,21398 . .21662,21795 . .21897,21973 . .22195)
/gene="F14G16.2"
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13864. .14927
/note="T32N15_del_retroTn"
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12735. .13052
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/note="T32N15_del_retroTn"
complement(12310. .15735)
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/note="T32N15_del_retroTn"

12162. .12238

/note="T32N15_del_retroTn"
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15224. .15350
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15024. .15226
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13087. .13862
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/note="F14G16" 7738. .7837 /note="F14G16" 7701. .7747

/note="F14G16" 7835. .8136

/note="F14G16" 8114. .8270

/note="F14G16"

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6002.

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/note="F14G16" 5887. .6013 /note="F14G16" 5241. .5443

'note="F14G16"

5136.

'note="F14G16"

2826.

note="F14G16"

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/note="F14G16" 2465. .2565

'note="F14G16"

note="F14G16" 1996.

/note="F14G16" 2793. .2826

note="F14G16"

/note="F14G16" 7300. .7710

repeat\_region repeat\_region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Levis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Martinez,E., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Wickerson,E., McLeod,M.P., Wadoor,M., Weigen,N., Wickerson,E., Newtson,N., Dulles,M., Ren,Y., Peters,L., Pickens,R., Prinus,E., Pu,L.L., Oulles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Sott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Sussani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Warfen,A., Washington,S., Walliams,G., Williams,A., Marren,R., Washington,S., Watlington,S., Wulliams,G., and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baylor Plaza, Houston, TX 77030, USA
On Jun 18, 2002 this sequence version replaced gi:19525901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-MAR-2002) of Molecular and Human G Baylor Plaza, Houston, T 3 (bases 1 to 120885)
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                                                                                                                                                     arbitrary. Gaps he runs of N, but the This record will
                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                   as soon as it is
be preserved.
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                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 57067 bases at least Q40 Consensus quality: 59738 bases at least Q30 Consensus quality: 62357 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: GSDR Center clone name: CH230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid;
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                                Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhäj,C., Escotto,M., Earnhart,C., Edgar,D., Fewards, C.C., Elhäj,C., Escotto,M., Falls,T., Ferraguto,D., Flagy,M., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunrathe,P., Hale,S., Hamilton,K., Gunrathe,P., Gun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-8L7, 63 unordered pieces.
                                                                                                                                                                                                                                             Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                            Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C. Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
                                                                                                                                                                                                                            Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J.,
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,P., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Massey,E., Mawhiney,E., McLood,M.P., Meador,M., Moi,G., Mctzkor,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: onsists of 63 contigs. The true order of the pieces
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* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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AC099720
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                     Db 133930
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-823-649A-6 (1-11) x AC095167 (1-185133)
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                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                     CTGACACAAAGAGTGGGGTTGAGTGTCTCTGAA 133898
                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerLysArgIleGlyLeuSerValSerGlu 11
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
                                                                                                 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bouslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gaye,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pherre,N., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pherre,N.,
                                                                                                                                                                                                    Mummalia; Eutheria; Rodentia; Sciurognathi; Mu
1 (bases 1 to 189300)
Birren.B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-415H15
                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                        unordered pieces.
AC099720
                                                                                                                                                                                                                                                                                                                              AC099720 189300 bp Mus musculus clone RP23-415H15,
                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                              AC099720.1 GI:16974219
                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                (bases 1 to 189300)
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of 2635
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HTG 18-NOV-2001 NCE, 10

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17630 17730 14207 16030 16130

10898 10998 12770 12870 14107

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40837 42821 42728 47163 47163 47163 47163 471194 49118 49118 49118 53245 53245 53345 53345 53345 53345 53173 55173 55173 58134 61217 61317 61317 61317 61317 61317 61317

72499 72599 75292 75392 77964

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-NOY-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 183000; agarose-fp
Insert size: 188400; sum-of-contigs
Quality coverage: 6.8 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 186360 bases at least Q40 consensus quality: 187869 bases at least Q30 consensus quality: 188281 bases at least Q20 consensus quality: 188281 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing vector: Plasmid; n/a; 100% of Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L17702
Center clone name: 415_H_15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99822 99921: gap of 100 bp 109922 116348; contig of 16427 bp in length 116349 116448; gap of 100 bp 116449 138337; contig of 21789 bp in length 138238 138337; gap of 100 bp 138238 138337; gap of 100 bp 1099244 16424 1642743; contig of 47406 bp in length 138234 1642743; contig of 47406 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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81895 90181; contig of 8287 bp in length
90182 90281; gap of 100 bp
90282 99821; contig of 9540 bp in length
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                                                                                                                                                                     clone_end:SP6
                                   18506. .20378
                                                                                                                              vector_side:left"
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                    /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RP23-415H15"
                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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81794: contig of 61316 bp in length
81894: gap of 100 bp
90181: contig of 8287 bp in length
                                                                                                                                                                                                                                           .16989
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                                                                                                      .18405
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Query Match:
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                   repeat_unit
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                                                                                                                                                   Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV16 at the 5' end and an overlap with ATCHRIV18 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA chromosome AL161505
                                                                                                                                                                                                                                                                            lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Camb
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich,
                                                                                                                                                                                                                                                                                                                                         Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R., Lamar, B., Stoneking, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 1; 6303 to 175721)
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                                                                                                                                                                                                                                                               E-mail: michael.bevan@bbsrc.ac.uk
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90282. .99821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
81895. .90181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:right"
35220 c 35414 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
185844. .189300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
138338. .185743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
99922. .116348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20479.
                                   /db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment
/note="F14G16"
                                                                              /variety="Columbia'
                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.00
90.91%
72.73%
83.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:7267326
                                                                                                                        .198176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.48e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .138237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .81794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35414 g 59994 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198176 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stumpf, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA linear PLN 16 e 4, contig fragment No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mewes, H.W., Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 16-MAR-2000
                                                                                                                                                                                                                                                                                  Norwich, UK
                                                                                                                                                                                                                                                                                                   Cambridge
                                                                                                                                                                                                                                                                                                                                           E-mail:
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repeat\_unit

/note="F14G16"

repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	Tebear_mirc	50000 t 1001 t	repeat unit	repeat_unit	repeat_unit	repeat_unit
/note="T32N15_del_retroTn" 1026110435	/note="F14G16" 1025510398	/note="F14G16" 81148270	78358136	7138. 7837	710 CG	7300. 7710 7300. 7710 700+0==014616	/10/64 E14610 7139. 7282 /note="E1/616"	\"\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	7.0000 6.0013 58876013 7.000 8014016	/1000 Firesto 5241. 5443 /note="F14616"	/note="F14G16" 51365243 /note="F14G16"	/note="£14G16" 36024665	2826. 3501 2826. 3501	27900 27900 200100 #814616#	24742791 24742791 /note="R14616"	24.65 25.65	22132530 /note="F14G16"	19962315 19962316 /note="F14G16"	19752479 /note="F14G16"	19011977 /note="F14G16"	18242012 /note="F14G16"	16721814 /mote="F14G16"	16461907 /note="F14G16"	15611647 /note="F14G16"	15281684 /note="F14G16"	970.0 997.1578 997.6="F14G16"	987. 1521 987. 1521	628 1027 628 1027 /note="F14G16"	591632 /note="F14G16"	492/94 /note="F14G16"	390448 /note="F14G16"	/note="F14G16"	/note="F14G16" 202 355	/note="F14G16" 216297	/note="F14G16" 190600	/note="F14G16" 121218	48 97
exon		intron	exon		intron		D 4			- <del>1</del> 44-5-5-4			CDS	gene	repeat	/ repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit		misc f	repeat unit	repeat unit	· reneat init	repeat unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	
2179521897 /gene="AII4g07310"	/gene=" <i>l</i> /number=	N ~	/gene="AT4g07310"	H D	. 615	/gene="AT4g07310"	CTAGTISTVEPDPDIPESNEIHEI"  21182	ERIGHT LEAT YOUR TOUR THE LEGISLAY I LIVE OF VEHICLE YEAR LIBERT OF FOUR YEARS OF THE TRUE	/ CLEAR CLEAR CLEAR CARRIED TO A CONTROL OF THE CON	/ COMUNITY OF THE PROPERTY OF	roteins, see	/gene="AN490/310" /note="contains similarity to Arabidopsis thaliana	/goinc/2.143907.2139821662,2179521897,2197322195)		_unit 1534015739 _note="T32N15 del									Ф 		/note="T3				/note="T32N15_del 1123111812	700Ce= 132N15	1086010959		108241086 /note="T32N1	10824 /note="T		/note="132N15_del_retroTn"

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US-09-823-649A-6 (1-11) x ATCHRIV17 (1-198176)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43645 CTTTCAAAACGAATTGGCGTGTCCGTGTCA 43616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hune,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Mahshari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. Buhay, C., Burch, P., Burkett, C., Burch, R., L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, J., Davis, C., Davy-Carroll, J., Davis, C., Davy-Carroll, J., Davis, C., Davy-Carroll, J., Davis, C., Davis, C., Davis, D., Davis, C., Davis, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gablsi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC114382.2 GI:21745644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC114382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 150018)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  norvegicus clone CH230-257F24, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(29065. .29454,29519. .29703,30603. 31062. .31307,31359. .31484))
/gene="AT4907320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(29065. .29454,29519. .29703,30603. .30969,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="AT4g07320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyproteins"
29065. .31484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pseudogene, similar to retrovirus-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AT4g07310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21898. .21972
/gene="AT4g07310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
90.00%
83.67%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:19263236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,JJ., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 38 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329 Consensus quality: 111894 bases at least Q40 Consensus quality: 116026 bases at least Q30 Consensus quality: 119751 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guverra, W., Gunarathe, P., Hale, S., Hamiton, K.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hornandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Tankson, T. F.,
T., Tankson, T. F.,
T
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 13, 2002 this sequence version replaced gi:18701531.
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 170083)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peters, L., Pickens, K., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojbokan, I., Rolfe, M., RRiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,K., Pace,A., Payton,B., Peery,J., Perez,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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Center project name: GNIF

Center clone name: CH230-155M2

Center clone name: CH230-155M2

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329

Consensus quality: 11169 bases at least Q40

Consensus quality: 11647 bases at least Q30

Consensus quality: 121122 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Levis, L.
Li J., Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lc ado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E.,
Ma.sshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Neytson, A., Nguyen, A., Nguyen, N.,
Nguyen, N., Viekerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pul, L., Ouiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sunton, A., Svatek, A., Tabor, P., Tamerisa, A., Tomass, N., Thomass, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Mard Moore, S., Warren, R., Washington, C., Watlitams, G., Williamson, A., Williams, G., Williamson, A., Williams, S., Worley, K.,
Weinstock, G. and Gibbs, R.
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                                                Baylor Plaza, Houston, TX //030, usa
On Jul 9, 2002 this sequence version replaced gi:17941157.
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                                                                                                                                        Submitted (10-JUL-2002) of Molecular and Human (
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Mammalia; Eutheria; Rodentia;
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                                                                                                       bmitted (10-JUL-2002) Human Genome Sequencing Center, Department Molecular and Human Genetics, Baylor College of Medicine, One ylor Plaza, Houston, TX 77030, USA
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Bryant,N.P.,
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COMMENT

bp in length

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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be preserved.
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Assembly program: Phrap; version 0.990329
Consensus quality: 12433 bases at least Q40
Consensus quality: 129469 bases at least Q30
Consensus quality: 134129 bases at least Q20
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Center clone name: CH230-3012
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Percent Similarity: 90.91% Conservative: 0

Best Local Similarity: 90.91% Mismatches: 1

Query Match: 97.96% Indels: 0

US-09-823-649A-7 (1-11) x AAT04800 (1-2631)

Qy 1 LeuAlaGlnAsnLeuAsnIle\*\*\*ArgLysGlu 11

Qy 1 LeuAlaGlnAsnLeuAsnIle\*\*\*ArgLysGlu 11

Db 2161 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 2193

Search completed: January 15, 2003, 12:56:57

Job time: 136.143 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Bucillus stearothermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity patent. EP 0875576-A 11 04-NOV-1998;
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Tan, T.C. and Phang, S.M.
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US-09-823-649A-7 (1-11) x AX002397
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Sequence 10 from Patent EP0875576
AX002397
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Bacillus stcarcthermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 0875576-A 9 04 NOV-1998;
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Bacillus Stearothermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 087576-A 10 04-NOV-1998;
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Sequence 9 from Patent EP0875576.
AX002396
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/db_xref="taxon:32644"
413 c 492 q 318
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351 c 401 g :
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Sequence 1 from patent US 6165765.
ARI. 765
ARI: 765.1 GI:14107000
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Hong, G.Ran., Huang, W.-h. and Zhai, F. deceased.
Bacillus stearothermophilus DNA polymerase with proof-reading 3'-5'
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AR053713
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Patent: US 5834253-A 1 10-NOV-1998;
Location/Qualifiers
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AR053714
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AR008369
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Best Local Similarity:
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Sequence 3 from patent US 6165765.
AR122766
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                         exonuclease activity
                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus DNA polymerase with proof-reading 3'-5'
                                                                                                                                                                                                                                                                                                                                                 Hong, G. Fan., Huang, W.-h. and Zhai, F. deceased
                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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Hong, G. and Huang, W.-h.
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1779 bp
16 from patent US 5753482
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415 c 487 g
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418 c 485 g
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Location/Qualifiers
1. .1779
                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae;
1 (bases 1 to 1779)
Ishino,Y., Uemori,T., Fujita,Y. and Katou,I.
DNA POLYMERASE GENE
Patent: JP 1993284971-A 1 02-NOV-1993;
TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                            Bacillus caldotenax.
Bacillus caldotenax
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E05777
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JP 1993284971-A/1.
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JP 1993284971-A/1
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ISHINO YOSHIZUMI, UEMORI
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/product='a DNA polymerase'

Location/Qualifiers
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425 c 529 g
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US-09-823-649A-7 (1-11) x E05777 (1-1779)
US-09-823-649A-7 (1-11) x AX002395 (1-1880)
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                                                                                                                                                                                                                                                          Bacillus stearothermophilus DNA polymerase I (klenow) clones including those with reduced 3'-to-5' exonuclease activity Patent: EP 0875576-A 8 04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                      unidentified
unidentified
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Method for cloning of a gene for Pol I type DNA polymerase
Patent: US 5436326-A 16 25-JUL-1995;
                                                                                                                                                                                                                                               UNIV SINGAPORE (SG)
                                                                                                                                                                                                                                                                                                         Tan, T.C. and Phang, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                 AX002395.1 GI:7241988
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Ishino,Y., Uemori,T.,
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425 c 529 g
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1. .1779
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486 c 573 g
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DNA POLYMERASE GENE
Patent: JP 1993304964-A 4 19-NOV-1993;
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Bacteria; Firmicutes; Bacillales; Geobacillus
1 (bases 1 to 2628)
                                                                                              Geobacillus stearothermophilus
Bacteria; Firmicutes; Bacillales; Geobacillus
1 (bases 1 to 2631)
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PN JP 1993304964-A/4
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JP 1993304964-A/4.
           Genet. Anal.
96303305
                                    Thermostable Bst DNA polymerase I lacks a 3'-->5' proofreading exonuclease activity
                                                                               Aliotta, J.M.,
                                                                                                                                       Geobacillus stearothermophilus
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ISHINO YOSHIZUMI, UEMORI TAKASHI, FUJITA YOSHIYO,
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Location/Qualifiers
1.2628
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/db_xref="taxon:1422"
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AUTHORS
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                                                                                                                                                           1 (bases 1 to 2631)
Ishino,Y., Uemori,T., Fujita,K. and Kato,I.
Method for cloning of a gene for pol I type DNA polymerase
Patent: US 5753482-A 13 19-MAY-1998;
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YELDHYEADD IIGTLAARAEQEGFEVKIISGDRDLTQLASRHVTVDLTKKGITDIEPY
TPETVREKYGLTPEQIYDLKGLMGDKSDNIPGYPGIGCLASRHVTVLKQFGTVENVLASI
DEVKCEKKLENLRGHRDLALLSKQLASICRDAPVELSLDDIVYEGQDREKYIALFKEL
GFQSFLEKMAAPAARGEKPLEBMEFAIVDVITEBMLADKAALVVEVMEENVHDAPIVG
IALVNEHGRFFMRPEFALADSQFLAMLADETKKKSMFDAKRAVVALKMKGIELRGVAF
                                                                            /organism="unknown"
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/db_xref="G1:1205984"
/translation="MKKKI.VLIDGNSVAYRAFFALPLI.HNDKG1HTNAVYGFTMMLNK
                                                                                                                                        Location/Qualifiers
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Maximum
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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  protein search, using sw model
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_urlus:*
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16: sp_bacteri
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Match
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Gapop 10.0 , Gapext
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49
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09x864 escherichia
09x864 escherichia
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0972j5 sulfolbus
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fusobacter	therm	campyloba	Q59599 neisseria g	Q9jxw8 neisseria m	Q8z2s2 salmonella	Q8rbe6 thermoanaer	đ	Q8u6f8 agrobacteri		Q9p8h9 emericella	Q9szd0 arabidopsis	Q8yqx3 anabaena sp	Q9jzul neisseria m	Q9bk02 tribolium c			ydra al	Q9w6v0 gallus gall	Q9w2j8 drosophila	Q8t9e7 drosophila	Q9df50 xenopus lae	067196 aquitex aeo	Q39130 arabidopsis		n8 arabidops	2 a	O22326 arabidopsis	5 chlamydia

## ALIGNMENTS

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RESULT 1
Q45458
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF00739; 5_3_exonuc_N; 1.
Pfam; PF00476; DNA, Pol_A; 1.
PrINTS; PF00476; DNA, POL_A; 1.
SMARR; SM00474; 35EXOC; 1.
SMARR; SM00474; 35EXOC; 1.
SMARR; SM00475; HhHZ; 1.
SMARR; SM00279; HhHZ; 1.
SMARR; SM00279; HHZ; 1.
SMARR; SM00279; DOLAC; 1.
TIGREAMS; TIGK00593; POLA; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
SEQUENCE 876 AA; 99008 MW; B981BCE
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InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR001098; DNA_pol.
InterPro; IPR002998; DNA_polI.
InterPro; IPR000291; Exo_N_I.
InterPro; IPR0003584; HHH_2.
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HSSP; P52026; 1XWL.
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Genet. Anal. 12:185-195(1996).
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             B981BCE95F1651A7 CRC64;
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Matches
                                                                                                                                                                                                                                                                                                  Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO. d68; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                         Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                  DNA polymerase I. POLA OR CPE1994.
                                                                                            01-MAR-2002 (TrEMBLrel 01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGR00593; pola; 1.

PROSITE; PS00447; DNA_POLYMERASE_A; 1.

SEQUENCE 877 AA; 99200 MW; 4B9639483FB41DHB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U93028; AAB62092.1; --
HSSB; P52026; IXML.
InterPro; IPR002562; 3.5_exonuclease.
InterPro; IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA polymerase I gene.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Fi
Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          024675;
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                                                                                                                                                   6MIX8Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLG1
                                                                                                                                    Q8XIW9;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Piam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu P., Leung C.H., Kong R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FW10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                     723 LAQNLNITRKE 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 LAQNLNITRKE 731
                                                                                                                                                                             ω
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                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01367; 5_3_exonuclease; PF02739; 5_3_exonuc_N; 1. PF004 6; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003584; HHH_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPR000513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001098;
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterologous expression of Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3_exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.0%;
                                                                                                                                                                                                                                                                                      98.0%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_polI.
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21,
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21,
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Last seq
                                                                                             Last sequence update)
Last annotation update)
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Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                                                                                                                      Score 48; DB 2; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                   866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                        RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,

ADomann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

AA Domann K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

AA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

AA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

AA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

AA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

AA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

AA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Yagquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

YC Comparative genomics of Listeria species.";

KL Science 294:849-852(2001).

Bristits Tinn600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                     Listeria innocua.
Bacteria; Firmicutes; Bacilius/Clostridium
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 866 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0668; DNAPCLI.
SMART; SM00275; 53EXOC; 1.
SMART; SM00275; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00882; POLIAC; 1.
TIGREAMS; TIGR00593; POLA; 1.
PROSITE; PS00447; DNA_POLYMERASE_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002298;
InterPro; IPR000513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U. EMBL; AP003192; BAB81700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=13 / TYPE
PubMed=11792842;
                      Listilist; LIN01600; ...
InterPro; IPR002421; 5.3_exonuclease.
InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_pol.
InterPro; IPR002298; EXO_N_I.
                                                                                                                                                                                                                                                                       Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
                                                                                                                                                                                                                                                                                      STRAIN-CLIP 11262 / SEROVAR 6A; PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q92BF0;
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Pfam; PF01367; 5_3_exonucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flesh-eater."
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 InterPro; IPRO
Pfam; PF01367;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              POLA OR LIN1600.
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InterPro; IPR001098; DNA_pol.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 LSQDLNISRKE 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LAQNLNIXRKE 11
              IPR003583; HHH_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         866 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 5_3_exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99118 MW; E7F786F720146615 CRC64;
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72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_poli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
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                                                                                                                                                                                                                                                                                                                                                                   group; Bacillales;
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Best Local
                    Matches
                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF02739; 5_3_exonuc
pfam; PF00476; DNA_pol_A;
SMART; SM00278; HhH1; 1.
                                                                                                                                        pfam; PF01367; 5_3_exonucleas
pfam; PF02739; 5_3_exonuc_N;
pfam; PF00476; DNA_pol_A; 1.
pRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                             Vazquez-Boland J.-A., Voss H., Wehland J., C "Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                            Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Cove E., de Daruvar A., Dehoux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRTAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN_1.
                                                                                                           SMART; SM00475;
SMART; SM00279;
                                                                                                                                                                                                  InterPro; IPR002562; 3.5_exonuclease. InterPro; IPR002421; 5_3_exonuclease. InterPro; IPR001098; DNA_pol. InterPro; IPR001298; DNA_polI.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21537279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase I. POLA OR LMO1565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9M9780
                                                                               PROSITE;
                                                                                       TIGRFAMs;
                                                                                                   SMART; SM00482;
                                                                                                                                SMART; SM00474;
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InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                   EMBL; AL591979; CAC99643.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBY6W6;
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1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                    Similarity
8; Conserv
                                                          proteome.
875 AA;
                                                                             pS00447; DNA_POLYMERASE_A; 1.
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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DNA_pol_A; 1.
                                                                                                           35EXOc; 1.
53EXOc; 1.
HhH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      SEROVAR . 1/2A;
                                                                                                  POLAC; 1.
                                                                                                                                                             _3_exonuc_N; 1.
                                                                                                                                                                      _3_exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11679669;
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                                                          98448 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%;
72.7%;
                             79.6%;
72.7%;
                                                                                                                                                                                        Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20,
20,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Pred. No. 15;
1; Mismatches
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                    ۲,
                             Score 39; DI
Pred. No. 15;
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                                                           94B541A6190D05CF CRC64;
                    Mismatches
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15;
                                        DB 16;
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                                                                                                                                                                                                                                                                                 Cossart P.;
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                    2;
                                    Length 875;
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,:
                    0;
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                    Gaps
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Q96LP7
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SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; POLAC; 1.
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01-JUN-2000 (TEMBLrel. 21, La:
01-JUN-2002 (TEMBLrel. 21, Las:
DNA polymerase I (EC 2.7.7.7).
POLA OR BH3153.
                                                                                                               Q96LP7 PRELIMINARY; PR"; 388 AA.
Q96LP7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01367; 5_3_exonuclease; 1. Pfam; PF02739; 5_3_exonuc_N; 1. Pfam; PF00476; DNA_pol_A; 1.
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STRAIN=C-125 / JC
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01-OCT-2000
                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR00593; pola; 1.

PROSITE; PS00447; DNA_POLYMERASE_A; 1.

Transferase; Nucleotidyltransferase; Complete proteome.

SEQUENCE 876 AA; 99545 MW; 3CA1D7EBDB689617 CRC64;
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Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
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HSSP; P52026; 2BDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                     Homo sapiens (Human)
                                                                                                         CDNA FLJ25320 fis, clone TST00267 (Fragment).
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SEQUENCE FROM N.A
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IPR000513;
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Pred. No.
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Q8VSV3
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Best Local :
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Q8VSV3;
01-MAR-2002
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Ishibashi T., Kanehori K., Takiguchi S., Kusano J.,
Hotuta T., Hiraoka S., Muzakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Suziyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.;
NEDO human cha Sequencing project.";
Submitted (OCT-2001) to the EMBI,/GenBank/DDBJ databases.
EMBI, AKO58049; BAB71440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown E.W., LeClerc J.E., Kotewicz M.L., Cebula T.A.;
"Three R's of bacterial evolution: how replication, repair,
recombination frame the origin of species.";
Environ. Mol. Mutagen. 38:248-260(2001).
EMBL; AF359695; AAL59502.1; -.
InterPro; IPR001098; DNA_pol.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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SMART; SM00482; POLAC; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN_1
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Q8VLLO;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001098; DNA_pol
Pfam; PF00476; DNA_pol_A; 1.
SMART; SM00482; POLAC; 1.
Q8VL18 PRELIMINARY, Q8VL18; 01-MAR-2002 (TrembLrel. 01-MAR-2002 (TrembLrel.
                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown E.W., LeClerc J.E., Kotewicz M.L., Cebula T.A. "Three R's of bacterial evolution: how replication, recombination frame the origin of species."; Environ. Mol. Mutagen. 38:248-260(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLA.
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EMBL; AF359736; AAL59543.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ECOR 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00476; DNA_pol_A; 1.
SMART; SM00482; POLAC; 1.
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MEDLINE=21610577; PubMed=11746762;
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8; Conserv
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Pred. No. 8.
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STRAIN=VARIOUS ST
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MEDLINE=21610577; PubMed=11746762;
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AF359702;
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AF359699;
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AF359696;
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AF359688;
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AF359680; AAL59487.1;
AF359681; AAL59488.1;
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                                       AAL59538.1;
AAL59539.1;
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AAL59517.1;
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RESULT
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SEQUENCE
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PROSTTE; PSO0715; SIGMA70_1; 1.

PROSITE; PS00716; SIGMA70_2; 1.

DNA-binding; DNA-directed RNA polymerase; Sigma factor;
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                                                                                                                                                                     Transcription regulation. SEQUENCE 281 AA; 31352 MW;
                                                                                                                                                                                                                                                                                                                                                                         clinical PCR development.";
Submitted (DEG-2000) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                Steiner B., Bowen M., Morrill W., Meyer R., "Random sequencing of Burkholderia pseudomallei strain 69313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                       InterPro; IPR000943; Sigma_70.
                                                                                                                                                                                                                                                                                      EMBL; AF326688;
HSSP; P00579; 1
                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES AND ATTACHMENT OF THE RNA FOLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-G9313
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_TaxID=28450;
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                                                                                                                            Local
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                                                                                  1 LAQNLNIXRKE 11
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L, AP359738; AAL59545.; -
L, AP359742; AAL59549.; -
L, AP359743; AAL59549.; -
L, AP359744; AAL59551.; -
L, AP359745; AAL59551.; -
L, AP359746; AAL59552.; -
L, AP359746; AAL59552.; -
L, AP359747; AAL59554.; -
L, AP359747; AAL59554.; -
L, AP359747; AAL59554.; -
L, AP359748; AAL59554.; -
L, AP359748; AAL59555.; -
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AF359738;
AF359739;
AF359742;
AF359742;
AF359744;
AF359744;
AF359745;
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                                                                                                             Similarity 7; Conserv
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Pred. No. 21;
2; Mismatches
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DT 01-OC
DT 01-DE
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Best Local
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Q8X8H1;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perna N.T., Pinkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; "Nature 409:529-533(2001).
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POLA OR Z5398 OR ECS4786.

Pocharichia coli 0157:H7.
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MEDLINE-2115631; PubMed-11258996;

Hayashi T., Makino K., Ohishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

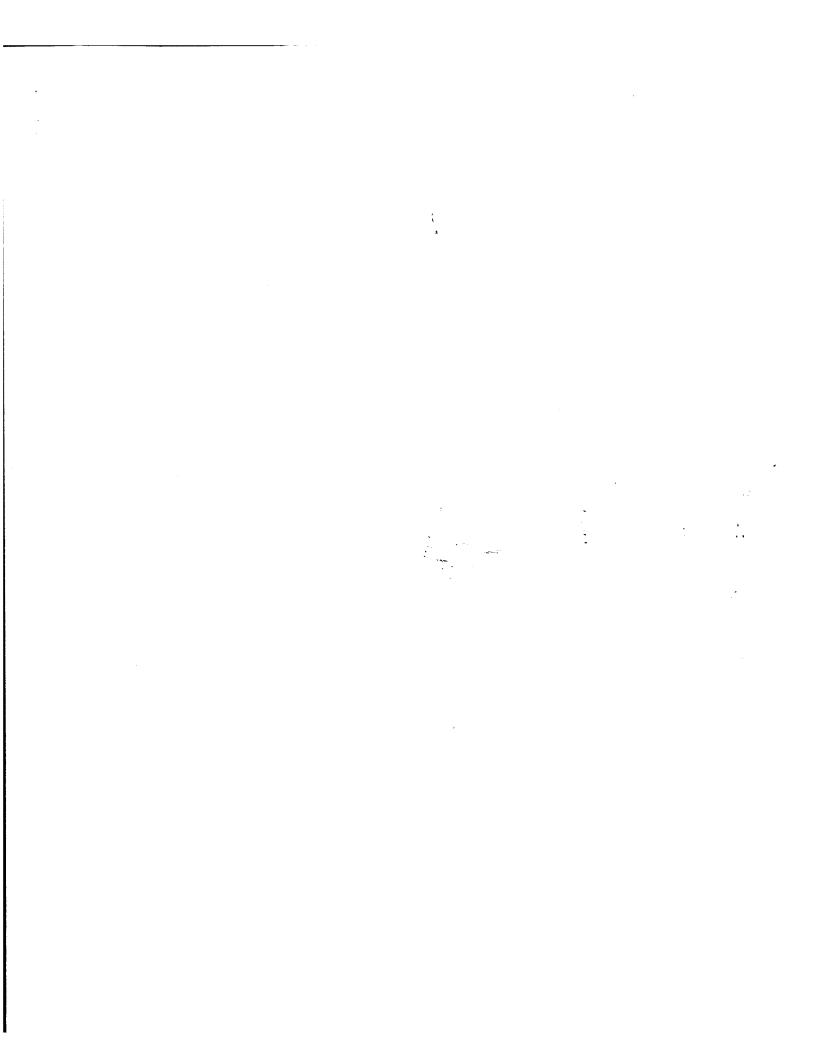
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Romplete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";
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01-JUN-2002 (TrEMBLrel.
DNA polymerase I, 3'-->
            077127;
01-027-2001 (TrEMBLrel. 18, Created)
01-027-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                   Q97L97
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MEDLINE=21074935; PubMed=11206551;
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ABC-type sugar transport system, permease component
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SM00475; 53EXOC; 1.
SM00279; HhH2; 1.
SM0028; POLAC; 1.
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PF01367; 5_3_exonuclease; 1.
PF02739; 5_3_exonuc_N; 1.
PF00476; DNA_pol_A; 1.
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8; Conserv
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IPR002298;
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IPR002421; 5_3_exonuclease.
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Pred. No. 68;
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Q972J5;
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01-JUN-2002
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109 AENLNIPREE 118
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"Tatusov R.L., Sabathe P., Dubois J., Qiu D., Hilli J., Wolf Y.I.,
Becnett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007582; AAK78642.1.
                                                                                             Prodom; PD000006; ABC_transportr; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_2.
ATP-binding; Hypothetical protein; Complete p
SEQUENCE 471 AA; 53267 MW; 570B89B1047DB5
                                                                                                                                                                                                                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Jin no K., Takahashi M., Sekine M., Baba S. I., Ankai A., Koshqi H., Hosoyama A., Fukui S., Naqazi Y., Nishijima K., Otsuka K., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-1., Mesuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00402; HPD_TRANSP_INN_MEMBR; Sugar transport; Complete proteome. SEQUENCE 289 AA; 32969 MW; 49DB3B01
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MEDLINE-21359325; PubMed-11466286;
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                                                                                                                                                                                                                                       DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66171.1; ~.
                                                                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=JCM 10545 / 7; PubMcd=11572479;
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                                                                                                                                                                                        InterPro; IPR003439; ABC_transportr. 7fam; PF00005; ABC_tran; 2.
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(TrEMBLiel. 19, Last sequence up)
(TrEMBLiel. 21, Last annotation
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66.78;
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Pred. No.
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Search completed: January 15, 2003, 12:36:11 Job time : 33.5714 secs



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Listing first 45 summaries
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MSAB_NEIGO
GAL1_YEAST
TACY_LISIV
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YRY5_CAEEL
Y554_AQUAE
ID12_RICCN
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DPO1_SALTY
CARB_NEIGO
CARB_NEIGO
RL29_RICCN
RL29_RICPR
Y773_METJA
ASNA_CLOPE
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BP28_DROME
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  N REF. 3/4).
                                                                                                                                                                                                                                                                                                                                                      # A REF. 3/4)
                                                                                                                                                                                                                                                                                                                                                                      3/4).
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  RESULT 2
DPO1_BACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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01-OCT-1993 (Rel. 2
15-JUN-2002 (Rel. 4
DNA polymerase I (E
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         EMBL; D12982; BAA02361.1; PIR; JX0256; JX0256.
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01-0CT-1993
                                                                                                                       -!- SUBUNIT:
                                                                                                                                                                                                                                NCBI_TaxID=1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                              BACCA
                                                                                                                              {DNA}(N)
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SEQUENCE FROM N.A., AND SEQUENCE MADLINE-93252765; PubMed-8486614; Uemori T., Ishino Y., Pujita K.,
                                                        This SWISS-PROF entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                     Uemori T., Ishino Y., Fujita K., Asada K., Kato I.; "Cloning of the DNA polymerase gene of Bacillus caldotenax characterization of the gene product."; J. Blochem. 113:401-410(1993).
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                           -i- FUNCTION: IN ADDITION TO FOLIMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.
-i- CATALYTIC ACTIVITY: N deoxymucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus caldotenax.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                  -i- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-i- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 27, Created)
. 27, Last sequence update)
. 41, Last annotation update)
(EC 2.7.7.7) (POL I).
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90.9%;
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A -> E (IN STRAIN USED IN REF. 3/4).

B Q -> R (IN STRAIN USED IN REF. 3/4).

I D -> E (IN STRAIN USED IN REF. 3/4).

T -> M (IN STRAIN USED IN REF. 3/4).

SV -> NA (IN STRAIN USED IN REF. 3/4).

R -> & (IN STRAIN USED IN REF. 3/4).

R -> & (IN STRAIN USED IN REF. 3/4).

R -> & (IN STRAIN USED IN REF. 3/4).

L -> V (IN REF. 2).

E -> & (IN REF. 2).

L -> V (IN REF. 2).
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G -> W (IN REF. 2).
S -> T (IN REF. 2).
RL -> SV (IN REF. 2).
V -> G (IN REF. 2).
E -> G (IN REF. 2).
T -> A (IN REF. 1).
T -> A (IN REF. 1).
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E -> K (IN REF. 2).
L -> V (IN REF. 2).
KW -> NG (IN REF. 2).
R -> AGV (IN REF. 2).
H -> Q (IN REF. 1).
QP -> HA (IN REF. 2).
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Pred. No. 0.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                  (See http://www.isb-sib.ch/announce/
                                                                      There are no restrictions
                                    Usage
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EF. 3/4).
EF. 3/4).
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                                      and for
                                                                                                EMBL outstation
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                                                                                                                collaboration
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RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alioni G., R Kunst F., Ogasawara N., Moszer I., Bloutin A., Borchert S., Bartero M.G., Bessieres P., Bolotin A., Borchert S., RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Borriss R., Boursier I., Brans A., Braun M., Brignell S.C., Bron S., Corles N., Carter N.M., Coloi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emnerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emnerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emnerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Enlizi A., Galleron N., Fitz C., Fulita M., Fulita Y., Fabret C., Ferrari E., Foulger D., Ra Fritz C., Fulita M., Fulita Y., Fabret C., Ferrari E., Foulger D., Fritz C., Fulita M., Fulita Y., Fabret C., Henaut A., Fritz C., Fulita M., Haga K., Haiech J., Harwood C.R., Henaut A., Filbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., All Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., All Hilbert H., Koetter P., Koningstein G., Krogh S., Kumano M., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., All Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., All Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 034996;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00476; DNA_POl_A; 1.
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuc_N; 1.
PRINTS; PR00868; DNAPOLI.
PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequencing and functional annotation in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPO1_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000513; Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lapidus A., Calleron N., Sorokin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r; SM00474; 35EXOC; 1.
r; SM00475; 53EXOC; 1.
r; SM00279; HhH2; 1.
r; SM00282; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002562; 3_5_exonuclease. IPR002421; 5_3_exonuclease. IPR001098; DNA_pol. IPR002298; DNA_polI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003584;
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877 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1;
Pred. No. 0.026;
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3'-5' EXONUCLEASE (BY SIMILARITY).
POLYMERASE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DASFC7F5B6DFA6F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlich S.D.;
n of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          880 AA
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       DAC TO
                                                                                                                 SMX4_SCHMA
                                                                                                                                     RESULT
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Q26603; 15-JUL-1999 (Rel. 15-JUL-1999 (Rel. 15-JUL-1999 (Rel.

Homeobox protein SMOX-4 (Fragment)

38, Created)
38, Last sequence update)
38, Last annotation update)

SMX4\_SCHMA

STANDARD;

PRT;

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B

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밁
                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; FOLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S. Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Scheer S., Scoffone F., Sekowska A., Seror S.J., Serror P., Schin B.S., Soldo I., Serokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognori A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzeneger T., Viari A., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H.F., Zunstein E., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., Tanaha R., Yoshikawa H.F., Zunstein E., Y
                                                                                                                                                                                                              TIGREAMS; TIGROUS93; pola; 1.
PROSTIE; PSO0447; DNA, POLYMERASE, A; 1.
PROSTIES; DNA directed DNA polymerase; DNA replication;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 880 AA; 99091 MW; AFB434AFDF26F488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00476; DNA_pol_A; 1.
Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuc_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000513; Exo_N_I.
InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SubtiList;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- function: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the Gram-positive bacterium Bacillus
725 LSQNLGITRKE 735
                                                1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P52026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF008220; AAC00350.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (N) {AND}
                                                                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002562; 3.
IPR002421; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002298; DNA_polI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohl T.M., Portetelle D., Porwollik S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG12656; polA.
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAB14869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         institutions as long as its content
                                                                                                                               79.6%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _5_exonuclease.
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                                                                                                                               Score 39; I
Pred. No. 2.
                                                                                                        Mismatches
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                                                                                                                                                           DB 1;
                                                                                                     2;
                                                                                                                                                        Length 880
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RESULT 5
CG12_YEAST ID CG12_Y 7
ID CG12_Y 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-FEB-1991 (Rel. 17, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gl/S-specific cyclin CLN2.
CLN2 OR YPL256C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bilateral metazoan.";
Mech. Dev. 38:25-32(1992).
                                                                                                                                                                                                                                                                              Hadwiger J.A., Wittenberg C., Richardson H.E., de Barros Lopes M., Reed S.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M85302; AAA29931.1; -. HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Hadwiger J.A., Reed S.I.; "Nucleotide sequence of the Saccharomyces cerevisiae CLN1 and
                                                                                                                                                                                                       "A family of cyclin homologs that control the G1 phase in yeast."; Proc. Natl. Acad. Sci. U.S.A. 86:6255-6259(1989).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; I
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P20438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG12_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Puerto Rican;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                   MEDLINE=90326560; PubMed=2197605;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89345642; PubMed=2569741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00024; HOMEOBOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Webster P.J., Mansour T.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92399260; PubMed=1356008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.6%;
63.6%;
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Pred. No.
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RESULT 6
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AB Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,

AB Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

AR Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

AB Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

A Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

Chung E., Churcher C.M., Coster F., Davis K., Duesterboeft A.,

Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterboeft A.,

A Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterboeft A.,

A Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterboeft A.,

A Hall J., Hebling U., Heumann K., Hilbert H., Hillier I.,

A Hall J., Hebling U., Heumann K., Johnston M., Kalman S., Kleine K.,

A Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

A Komp C., Kurdi C., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

A Komp C., Kurdi C., Lashkari D., Lew H., Lin A., Lin D., Couis E.J.,

A Marathe R., Messenguy F., Mewes H., W., Mirtipati S., Moesti D.,

A Marathe R., Messenguy F., Mewes H., W., Mirtipati S., Pearson D.,

Ba Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,

Cherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelln H.,
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
P00582;
21-JUL-1986 (Rel. 01, Created)
                                                            DPO1
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division
SEQUENCE 545 AA; 61696 MW; D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DEVELOPMENTAL STAGE: CLN1 AND CLN2 MRNAS FLUCTUATE PERIODICALLY IN THE CELL CYCLE, PEAKING IN G1 PHASE:
-1- MISCELLANEOUS: A DOMINANT MUTATION IN CLN2 GENE (CLN2-1), ADVANCES THE G1- TO S-PHASE TRANSITION IN CYCLING CELLS AND IMPAIRS THE ABILITY OF CELLS TO ARREST IN G1 PHASE IN RESPONSE TO EXTERNAL ABILITY OF CELLS TO ARREST IN G1 PHASE IN RESPONSE TO EXTERNAL
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"The nucleofide seconds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION. INTERACTS WITH THE CDC28 PROTEIN KINASE TO
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1
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Nucleic Acids Res. 18:4025-4025(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO04366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0006177; CLN2
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-1995) to the EMBL/GenBank/DDBJ databases
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"Structure of large fragment of Escherichia coli DNA polymerose complexed with dTMP.";
          Beese L.S., Friedman J.M., Steitz T.A.;
"Crystal structures of the Klenow fragment of DNA polymerase |
"complexed with deoxynucleoside triphosphate and pyrophosphate."
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"Escherichia coli DNA polymerase I. Sequence characterization and secondary structure prediction.";
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Biochemistry 32:14095-14101(1993).
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                                                      MED1.INE=94083412;
                                                                                                 Science
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                                                                                                                                                                                                                                                  MEDLINE-91114709; PubMed=1989886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic characterization of early
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-82120160, PubMed-6276402;
Joyce C.M., Kelley W.S., Grindley N.D.F.;
"Nucleotide sequence of the Escherichia coli polA gene and primary
structure of DNA polymerase I.";
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15-JUN-2002
                                                                                                                  "Structure of DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83189123;
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                                                                                                                                                                                                                                                                -RAY CHYSTALLOGRAPHY (2.6 ANGSTROMS)
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polymerase I (BC 2.7.7.7) (POL I).
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                                                                                                   260:352-355(1993).
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/ MG1655;
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                                                        PubMed=8260491;
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PDB; PDB; PDB; PDB; PIR;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brautigam C.A., Sun S., Piccirilli J.A., Steitz T.A.; "Structures of normal single-stranded DNA and deoxyribo-3'-s-phosphorothiolates bound to the 3'-5', exonucleolytic active s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDI.INE-99105320; PubMcd-9888810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 38:696-704(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural origins of the exonuclease resistance of a zwitterionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h. Biochem. Biophys. 301:174-183(1993).

FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA E EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY. IT TO UTILIZE NICKED CIRCULAR DUPLEX DNA AS A TEMPLATE AND UNMIND THE PARENTAL DNA STRAND FROM ITS TEMPLATE.

CATALITIC ACTIVITY: N deoxynucleoside Lriphosphate = N d
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J01664; AAA24404.1;
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Pfam; Pr01612; 3_5_exonuclease; 1.
Pfam; Pr02773; 5_3_exonuc_N; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY. THIS DNA POLYMERAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (BC 2.7.7.7) (POL I).
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Pfam; PF00476; DNA_pol_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLA OR LL2142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CDS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPO1_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LAQNLNIXRKE 11
                                                                                                                                                                                       SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                         + {DNA}(N).
SUBUNIT: SI
                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                               FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LARQUNIPRKE 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003583; HHH_1.
IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002562; 3_5_exonuclease.
IPR002421; 5_3_exonuclease.
IPR001098; DNA_pol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002298; DNA_polI.
IPR000513; Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclease; Exonuclease; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polA.
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517
928
928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1;
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5'-3' EXONUCLEASE.
3'-5' EXONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLENOW FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D-structure;
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Вb
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                J. Bacteriol. 179:4473-4479(1997).

-i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY,
EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
                                                                      entities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MC1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DNA polymerase I (EC 2.7.7.7) (POL I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; Hydrolase; Exonuclease; DNA-binding; Complete proteome. SEQUENCE 877 AA; 98732 MW; A5C2BEB92FF98FB2 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00476; DNA_pol_A; 1. Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_pol1.
InterPro; IPR000513; Exo_N_I.
InterPro; IPR003594; HHH_2.
                                EMBL; U78771; AAB64184.1; HSSP; P52026; 1XWL.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE~97369814; PubMed=9226255;
                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPO1
                                                                                                                                                                                                                                                                                                         "Characterization of Lactococcus by ISS1 transposition.";
                                                                                                                                                                                                                                                                                                                                        Duwat P., Cochu A., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS; TIGRO0593; pola; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROO868; DNAPOLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; 1PR002421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          722 LARNLGITRKD 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LAQNLNIXRKE 11
                                                                                                                                                                                  + {DNA}(N).

SUBJUNT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.

SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                          SIMILARITY).

CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _LACLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P52026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE006442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
IPR002562; 3_5_exonuclease. IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK06240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3_5_exonuclease
5_3_exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3_exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                          lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877
                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 877
                                                                                                                                                                                                                                                                                                                          A.;
UV-sensitive mutants obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                  ACTIVITY
                                                                                                                                                                                                                                                                             THIS
                                                                                                                                                                                                                                                                 DNA POLYMERASE
( BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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InterPro;

EMBL outstation a collaboration

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RRA Mooney P. Moule S., Mones M., Leather S., McDonald S., McLean J., McMand M., Mooney P. Moule S., Mungall K., Murphy L., Niblett D., Odell C., RRA Mooney P. Moule S., Mungall K., Murphy L., Niblett D., Odell C., RRA Motherford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch E., RRA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Rabelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Raw Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Raw Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Raw Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Raw Weltjens I., Eeck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Thomas S., Lelaure V., Mottier S., Ra Galibert F., Aves S.J., Xiang Z., Taylour S., Lelaure V., Mottier S., And Lucas M., Rochet M., Galillardin C., Tallada V.A., Gazzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., And Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J., Forsburg S.L., Van Cerrutti I. L. (John T., Moreno S., Armstrong J.,
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Pfam; PF00476; DN
Pfam; PF01367; 5_
Pfam; PF02739; 5_
PRINTS; PR00868;
                                                              Cerrutti L. Lowe T., McCombie W.R., Paulse I., Potts Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q10086;
01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAO7_
              -!- SUBCELLULAR LOCATION: Nuclear (Probable)
-!- SIMILARITY: CONTAINS 1 2N(2)-CYS(6), FUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative transcriptional regulatory protein C11D3.07c. SPAC11D3.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHPO
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.

Transferase: DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
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; SM00475; 53EXOC; 1.
; SM00279; HhH2; 1.
; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877 AA; 98895 MW; EA803CD55BA9F620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exonuclease; DNA-binding
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; 5_3_exonuclease;
; 5_3_exonuc_N; 1.
68; DNAPOLI.
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Pred. No.
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                FUNGAL-TYPE BINUCLEAR
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                                                                                                                                                  Potashkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jagels K.,
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Best Local Similarity
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                                                                                                                                                                                       MEDLINE=21357209; PubMed=11463916; Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam L.A., White N., Wolf A.M., Utterback R.R., Hansen C.i., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ul-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
POLA OR SP0032.
                                 Science 293:498-506(2001).

-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONUCLEASE ACTIVITY.

-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + (DNA)(N).

-!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lopez P., Martinez S., Diaz A., Espinosa M., Lacks S.A.; "Characterization of the polA gene of Streptococcus pneumoniae and comparison of the UNA polymerase I it encodes to homologous enzymes from Escherichia coli and phage Ty."; J. Biol. Chem. 264:4255-4263(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
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DNA_BIND 7 34 ZN(2)-CYS(6), FUNGAL-TYPE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jopez P., Martinez
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SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
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PS50048; ZN2_CY6_FUNGAL_2; 1.
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its

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                                                                                   STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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   Adams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
George R.A., Lewis S.E., Richards S., As
                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical CG10805,
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                                                               Adams M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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IPR002298; DNA_polI
IPR000513; Exc_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003584; HHH_2
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IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR00593; pola; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
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5_3_exonuc_N; 1.
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63.6%;
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D -> E (IN REF 1).
V -> M (IN REF 1).
SES -> AEG (IN REF 1).
SES -> A (IN REF 1).
V -> Å (IN REF 1).
K -> Q (IN REF 1).
M -> V (IN REF 1).
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R -> Å (IN REF 1).
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   Evans C.A., Gocayne J.D.,
I., Hoskins R.A., Galle R.F.
Ashburner M., Henderson S.
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Felstchmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,

RA Jalaii M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA McIntosh M., Mishina N.V., Mobarry C., Moris J., Moshrefi A.,

RA Mount S.M., Myo M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Mount S.M., Myo M., Murphy B., Mrphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Siden K.A., Nixon K., Sungski M.P., Shin H.,

RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Slapleton M., Strong R., Sin E.,

RA Wang Z.-V., Wassaarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-V., Wassaarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-V., Wassaarman D.A., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunnes M., Dugan-Rocha S., Dunkov B., Dunkov B., Dunkov B., Dunkov B., Dunkov B., Dunko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                               EMBL; AE003615; AAF52447.2;
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                                                                                                                                                                                                                                                                                                                                                            license agreement (See http://www.isb-sib.ch/announce/
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ng as its content is in no
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Qy Matches Query Match SEQUENCE Hypothetical protein PROSITE; FlyBase; REPEAT InterPro; IPRO00357; HEAT\_repeat 510 LLQNLNVTKK 519 Local 1 LAQNLNIXRK Similarity 6; Conserv PS50077; HEAT\_REPEAT; FALSE\_NEG FBgn0031864; CC10805 2096 AA; Conservative 10 2094 69.4%; 60.0%; 237217 WW. Score 34; Pred. Mismatches 3E7B3C67CE6DF62C CRC64; NO. 61; DB 1; Length 2096; Indels 0;

0;

P25823; 01-MAY-1992 01-MAY-1992 15-JUN-2002

(Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 41, Last annotation update)

Drosophila melanogaster (Fruit fly)

Maternal tudor protein.

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TUD\_DROME RESULT 12

TUD\_DROME

STANDARD;

2515 AA

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15-JUN-2002 (Rel. 41, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
-1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
-1- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Golumbeski G.S., Bardsley A., Tax F., Boswell R.E.; "Tudor, a posterior-group gene of Drosophila melanogaster, encodes novel protein and an mRNA localized during mid-oogenesis."; Genes Dev 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
SEQUENCE FROM N.A.
                             Clostridium
                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                               Plasmid pCP13
                                                         Clostridium perfringens
                                                                            Hypothetical protein PCP12
                                                                                                                    Q93MD5;
                                                                                                                             YU12_CLOPE
                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00333;
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; iPR001097; Maternal_tudor.
InterPro; iPR002999; Tudof.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X62420; CAA44286.1; PIR; A41519; A41519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
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                  NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                            Developmental
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                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00567; TUDOR; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
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2451
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60.0%;
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TUDOR
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-Jul-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein AF1257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YC57_ARCFU
029011;
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                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(200-i-SIMILARITY: To C.perfringens pIV404 ORF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashito
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.
"Complete genome sequence of Clostridium perfringens, an
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                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Archaeoglobi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003515; BAB62450.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LAEELNVTRSE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE UPF0020 FAMILY.
AE001017; AAB89985.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   il protein; Plasmid; Complete proteome.
161 AA; 19180 MW; DBE5BE41BBE4CEDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on
                                                                                                                                                                       There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲.
                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamashita A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaerobic
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                                                                                                                 for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       incorporation of labeled ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exonuclease activity during DNA sequencing from a template and the polymerase excises mismatched nucleotides from the 3' terminus at a faster rate than it removes correctly matched nucleotides. The polymerase is used particularly for DNA sequencing, also for filling in 5' overhangs, synthesis of DNA DNA sequencing, also for filling in 5' overhangs, synthesis of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase that is modified (see AAY91930) so that during DNA sequencing, it effectively incorporates all four fluorescent dyedideoxynucleotide triphosphates (ddNTP), or their analogs, and recommendations of the contraction of the contra
                                                        02-MAR-2000; 2000US-0517871
                                                                                                28-FEB-2001; 2001WO-US06571.
                                                                                                                                      07-SEP-2001.
                                                                                                                                                                              WO200164954-A1
                                                                                                                                                                                                                  Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus (Bst) DNA polymerase 1 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                   AAE11060;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE11060 standard; Protein; 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 82-90; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA polymerase, useful particularly in DNA sequencing, incorporates all four dideoxynucleotide triphosphate terminators with about equal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA08545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200017330-A1
                     (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                          Bst; enzyme; amplification; hybridisation.
                                                                                                                                                                                                                                                                           Reverse transcription; DNA polymerase 1; Bacillus stearothermophilus,
                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 LAQNLNITRKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the discrimination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence shows a wild type Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-283563/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by random primer labeling and in site-directed mutagenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0157397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-IB00146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "F421Y in AAY91930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               observed with the unmodified enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 21; Length 587; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and reduces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dye-labeled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QУ
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RESULT 8
AAR80140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                          24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary strands. The present sequence is Bacillus stearothermophilus (Bst) DNA polymerase 1 protein fragment which lacks 5' to 3' exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus; thermostable DFT polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme
                                                                                                  N-PSDB; AAT04803.
                                                                                                                           WPI; 1995-373510/48
                                                                                                                                                                                        Riggs MG,
                                                                                                                                                                                                                                                 (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.stearothermophilus DNA polymerase encoded by clone 8st3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR80140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR80140 standard; Protein; 588 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to reverse transcription of RNA templates using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 29; Fig 10; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-589872/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 LAQNLNJTRKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang F, Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD18459.
                                                                                                                                                                                    Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                       95US-0394232
94US-0222612
                                                                                                                                                                                                                                                                                                                94US-0307410
                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US04080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
The present sequence plan sequencing, effectively DNA polymerase that, during DNA sequencing, effectively incorporates all four fluorescent dye-labeled dideoxynucleotide triphosphates (ddNTP), or their analogs, and reduces the discrimination, triphosphates (ddNTP), or their analogs, for incorporation of labeled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene (AAT04801) to remove a 195 bp HincII-PyuII fragment from the region encoding the 5'-3' exonuclease. The deleted fragment removes 65 amino acids (residues 178-242 of the protein) including 2 Gly residues though to correspond to 2 amino acids in the E.coli DNA polymerase I necessary for 5'-3' exonuclease activity. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain
                                                                                                                                                                                                                                          Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the modified Bacillus stearothermophilus thermostable DNA polymerase encoded by the clone Bst3 which contains a deletion in the 5'.3' exonuclease domain. The corresp.
                                                        The present sequence shows a modified Bacillus stearothermophilus DNA polymerase that, during DNA sequencing, effectively
                                                                                                   Claim 7; Page 95-103; 109pp; English.
                                                                                                                                              New DNA polymerase, useful particularly in DNA sequencing, incorporates all four dideoxynucleotide triphosphate terminators with about equal
                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. stearothermophilus 320 modified DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene was constructed by digestion and recombination of the full length
                                                                                                                                                                                             N-PSDB; AAA08544
                                                                                                                                                                                                                                                                         (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                     21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                    14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                 WO200017330-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                random primer labeling; site-directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY91930 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 LAQNLNITRKE 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LAQNLNIXRKE 11
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                                                                                                                                                                                                             2000-283563/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 87-90; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase; DNA sequencing; 3' to 5' exonuclease activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                     98US-0157397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "F422Y substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "wild type sequence is Leu-Glu-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 588 AA
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                            from wild type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 588;
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       The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactionwyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary extrande The PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exconuclease activity during DNA sequencing from a template and the polymerase excises mismatched nucleotides from the 3' terminus at a faster rate than it removes correctly matched nucleotides. The polymerase is used particularly for DNA sequencing, also for filling in 5'-overhangs, synthesis of DNA probes by random primer labeling and in
                                                                                                                                                                                                                                                                   Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reacting buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                     Claim 7; Fig 6; 118pp; English.
                                                                                                                                                                                                                                                         obtain cDNA
                                                                                                                                                                                                                                                                                                                                                                                             Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                                              (PROM-) PROMEGA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoactinomyces vulgaris Tvu DNA polymerase T289M truncated mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                         2001-589872/66.
                                                                                                                                                                                                                                                                                                                                                                                             Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification; hybridisation; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                           AAD18445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 588 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                             Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by A1'G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; Thermoactinomyces vulgaris; Tvu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
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strands. The

present sequence is Thermoactinomyces vulgaris Tvu DNA

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Best Local :
                                       Query Match
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    Matches
                                                                                                                                     polymerases derived from hyperthermophilic eubacteria, in particular, polymerases derived from hyperthermophilic eubacteria, in particular, a purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase having DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Tvu DNA polymerase can be used for processes of high temperature nucleic acid amplification and sequencing without substantial loss of DNA synthesis activity. The enzyme can be used to perform high temperature reverse transcription in the absence of manganese ions and in high throughput robotically-manipulated procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary structure is removed or limited. The present sequence represents the amino acid sequence of a 5'-3' exonuclease deletion mutant form of the process of the present sequence and the process of the secondary structure is removed or limited. The present sequence represents the manipulant and polymerase, reverse transcription of the present sequence represents the manipulant and polymerase transcription in the secondary structure is removed or limited. The present sequence represents the manipulant and polymerase and polymerase transcription in the secondary structure is removed or limited. The present sequence represents the manipulant polymerase and polymerase transcription in the secondary security.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase T289M truncated mutant. This Tvu T289M mutant is obtained by deleting 288 amino acids from the N-terminal end of wild-type T.
                                                                                  Sequence
                                                                                                                       Tvu DNA polymerase called T289M.
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides compositions comprising thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Fig 8; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplification, reverse transcription and sequencing reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulgaris for us in many recombinant DNA techniques, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel thermostable DNA polymerase derived from Thermoactinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH47392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deletion mutant; T289M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tvu DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable; DNA polymerase; hyperthermophilic; DNA synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tvu DNA polymerase deletion mutant T289M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulgaris Tvu DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROM-) PROMEGA CORP.
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Local Similarity
es 10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang F, Hartnett JR;
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                                                                                  588 AA;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid amplification; reverse transcription;
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                  90.98;
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Pred. No.
                    Score 48;
Pred. No.
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    Mismatches
                  DB 22; Length 588;
0.2;
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  <u>ب.</u>
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                                                                                              RESULT 13
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                                                                                                                                                                                                Matches
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                          This is the protein sequence (589 amino acids) of the Bacillus stearothermophilus strain DNA polymerase. The heat stable DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in amethod for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
                                                                                                                                                                                                                                                                                                                                                                                                                          mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt DNA} polymerase from Bacillus stearothermophilus - used in {\tt DNA} amplification and sequencing methods having lower frequency o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW30094 standard; Protein; 589 AA.
            30-MAY-1996 (first entry)
                                                                   AAR80141 standard; Protein; 590 AA
                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Pages 29-30; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-474304/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus stearothermophilus; DNA polymerase; DNA amplification; DNA replication; exonuclease; proof reading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus DNA polymerase (peptides 1-589).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW30094;
                                          AAR80141;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT90820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hong GF, Huang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZHAI/) ZHAI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUAN/) HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HONG/) HONG G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1996;
18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1998 (first entry)
                                                                                                                                      434 LAQNLNITRKE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 LAQNINITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LAQNLNIXRKE 11
                                                                                                                                                                  1 LAQNLNIXRKE 11
                                                                                                                                                                                                              ocal
                                                                                                                                                                                               10;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                    589 AA;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0544643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0160402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0642684
                                                                                                                                                                                                          98.0%;
90.9%;
                                                                                                                                                                                                        Score 48; DB
Pred. No. 0.2;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                       DB 18; Length 589;
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0

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RESULT 14
AAE11057
ID AAE11
XX AAE11
XX AAE11
XX AAE11
XX Therm
DY 18-DE
XX Therm
XX Rever
XX Rever
XX enzym
XX Therm
OS Therm
OS Therm
OS Synth
XX WO20C
XX WO20C
XX O7-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the modified B.stearothermophilus thermostable DNA polymerase encoded by the clone Bst4. This clone encodes the sequence of a natural degradation product obtained when the DNA polymerase clone Bst3 (AAT04803) is expressed in E.coli. The same sequence is found when the full length clone (AAT04801) is expressed and cleaved with subtilisin to produce a "Klenow-type" DNA polymerase. This sequence starts with the Val residue at pos. 28 of the full length protein. This contrasts with a commercially available B.stearothermophilus DNA polymerase subtilisin fragment where the protein sequence starts with the Val account of the sequence starts with the Val account of the sequence starts with the NA polymerase subtilisin fragment where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-1995;
01-APR-1994;
16-SEP-1994;
       07-SEP-2001
                                                                               Synthetic.
                                                                                           Thermoactinomyces vulgaris
                                                                                                                                Reverse transcription; DNA polymerase; Thermoactinomyces vulgaris; Tvu; enzyme; amplification; hybridisation; mutant; mutein.
                                                                                                                                                                                                                                                                  AAE11057;
                                          WO200164954-A1
                                                                                                                                                                                      Thermoactinomyces vulgaris Tvu DNA polymerase M285 truncated mutant.
                                                                                                                                                                                                                                                                                                 AAE11057 standard; Protein; 592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence starts with the Ala residue corresp. to pos. 290. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 92-94; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.stearothermophilus DNA polymerase encoded by clone Bst4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus DNA encoding thermostable polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT04804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                 435 LAQNLNITRKE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for nucleic acid sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-373510/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0394232.
94US-0222612.
94US-0307410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US04080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
   RESULT 15
AAB85950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Gu T,
                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                            AAB85950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
Huang F,
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at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium in reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary strands. The process sequence is Thermoactinomyces vulgaris Twu DNA polymerase M285 truncated mutant. This Tvu M285 mutant is obtained by deleting 284 amino acids from the N-terminal end of wild-type T. vulgaris
                                                                                                                                                                                                                                                                           Tvu DNA polymerase; deletion mutant; M2
                                                                                                                                                                                                                                                                                         Thermostable; DNA polymerase; hyperthermophilic; DNA synthesis; Tvu DNA polymerase; nucleic acid amplification; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermostable DNA polymerase such as Thermoactinomyces vulgaris (\tau vu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse transcription of RNA using "Yu and Bst DNA polymerase, comprises combining the polymerase, KNA containing sample, a prime reaction buffer having magnesium ions and reacting the mixture to
                                                                         02-MAR-2000; 2000US-0517439
                                                                                                                  28-FEB-2001; 2001WO-US06436
                                                                                                                                                                                                  WO200164838-A2
                                                                                                                                                                                                                                     Thermoactinomyces vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 4; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                        Tvu DNA polymerase deletion mutant M285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB85950 standard; Protein; 592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to reverse transcription of RNA templates using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000; 2000US-0517871.
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                                       (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tvu DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 LAQNINITIKKE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repetitive heating/cooling cycles without the requirement of fresh enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Hartnett JR;
                                                                                                                                                                                                                                                                               M285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 0.2;
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and

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Search completed: January 15, 2003, 11:20:24
Job time: 31.2857 secs
                                                                                            В
                                                                                                                                     γQ
                                                                                                                                                                                                                                                                                                                               The invention provides compositions comprising thermostable DNA

Coplymerases derived from hyperthermophilic eubacteria, in particular,

Ca purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase

Chaving DNA synthesis activity. It is useful for determining the

Can incleotide base sequence of a DNA molecule. Tvu DNA polymerase can be

cused for processes of high temperature nucleic acid amplification and

cused for processes of high temperature reverse transcription in the

can be used to perform high temperature reverse transcription in the

can be used to perform high temperature reverse transcription in the

cused sequence of manganese lons and in high throughput robotically manipulated

cused correctures because greater enzymatic stability is retained at room

cused the transcription of temperature. Using the Tvu DNA polymerase, reverse transcription

cused to procedures because greater enzymatic stability is retained at room

cused to procedure is removed or limited. The present sequence represents the

cushon acid sequence of a 5'-3' exonuclease deletion mutant form of
                                                                                                                                                                             Query Match 98.0
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 6; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including amplification, reverse transcription and sequencing reactions -
                                                                                                                                                                                                                                                                                                                     Tvu DNA polymerase called M285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH47392.
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                                                                                     437 LAQNINITRKE 447
                                                                                                               1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                        592 AA;
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90.9%;
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                                                                                                                                                                             Indels
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Minimum DB seq length: 0
Maximum DB seq length: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                            Score
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       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
       US-09-057-969-7
US-09-057-969-6
US-09-057-969-4
US-09-057-969-4
US-09-057-969-4
US-08-436-644-23
US-08-436-644-23
US-08-137-871-2
PCT-US95-04080-23
US-09-157-97-1
US-09-157-97-4
US-08-34-232A-25
US-08-34-232A-25
US-08-34-232A-25
US-08-34-232A-25
US-08-34-2-684-4
US-08-34-2-684-4
US-08-34-2-684-2
US-09-157-871-6
PCT-US95-04080-25
US-09-157-871-64-27
US-09-157-642-27
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US-09-157-643-27
US-09-157-871-871-4
US-08-34-232A-27
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US-09-457-963-17
US-09-457-963-17
US-09-457-963-17
US-09-578-963-17
US-09-578-963-17
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US-09-578-968-3
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Sequence 4, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 3, Appli
Sequence 2, Appli
                                                                          Sequence 4, Appli
Sequence 5, Appli
Sequence 25, Appli
Sequence 4, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
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Sequence 22, Appl
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
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Sequence 23, Appl
Sequence 23, Appl
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Sequence 6, Appli
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                  Qy
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US-09-057-969-7
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   1 LAQNLNIXRKE 11
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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US-09-057-969-2	US-08-428-823-14	US-08-208-036-14	PCT-US95-04080-34	PCT-US95-04080-32	PCT-US95-04080-20	US-09-517-871-20	US-09-517-871-2	US-08-394-232A-34	US-08-394-232A-32	US-08-394-232A-20	US-09-135-642-34	US-09-135-642-32	US-09-135-642-20	US-08-436-664-34	US-08-436-664-32	US-08-436-664-20	US-08-633-476-2
Sequence 2, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 34, Appl	Sequence 32, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 2, Appli	`	-		Sequence 34, Appl	•	Sequence 20, Appl	Sequence 34, Appl	Sequence 32, Appl	Sequence 20, Appl	Sequence 2, Appli

ALIGNMENTS

## Query Match Best Local Similarity Matches 10; Conservative GENERAL INFORMATION: TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO: 7: REGISTRATION NUMBER: 32,147 REFERENCE/DOCKET NUMBER: 674 TELECOMMUNICATION INFORMATION: COMPUTER: IBM PC compa OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: ADDRESSEE: FROMMER LAWRENCE & HAUG LLP TOPOLOGY: linear MOLECULE TYPE: amino acid SEQUENCE CHARACTERISTICS: LENGTH: 294 amino acid TITLE OF INVENTION: TITLE OF INVENTION: ATTORNEY/AGENT INFORMATION: NAME: KOWALSKI, THOMAS J COMPUTER READABLE FORM: APPLICANT: PHANG, SENG MENG APPLICANT: TAN, TIEN CHYE NUMBER OF SEQUENCES: APPLICANT: WONG, VICTOR THI WONG APPLICATION NUMBER: US/09/057,969 FILING DATE: 09-APR-1998 CITY: NEW YORK STATE: NEW YORK STRANDEDNESS: CLASSIFICATION: COUNTRY: TELEPHONE: MEDIUM TYPE: 10151 amino acid Application US/09057969 745 FIFTH AVENUE 294 amino acids USA Patentin Release #1.0, Version #1.30 E: Floppy disk IBM PC compatible 212-588-0800 09-APR-1998 single BACILLUS STEAROTHERMAPHILUS DNA POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED 3'-TO-5' EXONUCLEASE ACTIVITY PC-DOS/MS-DOS 98.0**%**; 90.9**%**; 0; Score 48; DB 3; Pred. No. 0.024; 674507-2001 Mismatches DB 3; Length 294; 0

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US-09-057-969-6

109 LAQNINITRKE 119

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                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                              Sequence 5, Application US/09057969 Patent No. 6013451
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                  CORRESPONDENCE ADDRESS:
                                                                                        TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO TITLE OF INVENTION: 3'-TO-5' EXONUCLEASE ACTIVITY NUMBER OF SEQUENCES: 17
                                                                                                                                                              APPLICANT: WONG, VICTOR TO APPLICANT: PHANG, SENG MED APPLICANT: TAN, TIEN CHYE
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CLASSTERON Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/057,969

FILING DATE: 09-APR-1998

CLASSTERON US/09-APR-1998
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TITLE OF INVENTION: 3'-To-5' EXONUCLEASE ACTIVITY

TITLE OF INVENTION: 3'-To-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 212-588-0800
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ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
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STRANDEDNESS: sir
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STATE: NEW YORK
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                                  STREET:
                                                    ADDRESSEE:
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10; Conserva
NEW YORK
                            745 FIFTH AVENUE
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IBM PC compatible
                                                  FROMMER LAWRENCE & HAUG LLP
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Pred. No.
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US-09-057-969-4
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GENERAL INFORMATION:
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              TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO: 4:
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NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 6745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0800
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TITLE OF INVENTION: BACTLLO
TITLE OF INVENTION: 9°CYMER
TITLE OF INVENTION: 3′TO-5
NUMBER OF SEQUENCES: 17
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                             REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 678
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-588-0800
TELEPHAX: 212-588-0500
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
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LENGTH: 457 amino acids
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CURRENT APPLICATION DATA:
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Local Similarity 90.9%;
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                                                                                                                      NAME: KOWALSKI, THOMAS J
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS STEAROTHERMAPHILUS DNA
POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
3'-TO-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
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                                                                                   674507-2001

 Mismatches

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; Sequence 23, Application US/08436664
; Patent No. 5874282
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                                                                                                                                                           Matches
                                                                                                                                                                                        Query Match
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                           NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
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                                                                                            432 LAQNLNITRKE 442
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                          1 LAQNINIXRKE 11
                                                                                                                                                         Local Similarity tes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/642,684
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LOCAL Similarity 90.9%;
les 10; Conservative
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                                                                                                                                                           Conservative
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FENG, ZHAI
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 Mismatches

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                                                                                                                                                                        Score 48; DB 2;
Pred. No. 0.049;
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                                                                                                                                                                                       DB 2; Length 587;
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                                                                                                                                                                        US-09-135-642-23
                                                                                                                                                                                                                                                                                                                                                               US-08-436-664-23
                                                                                                                      Patent No. 6066483
GENERAL INFORMATION:
                                                                                                                                                       Sequence 23,
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: NAME OF SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                 1 LAQNLNIXRKE 11
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ADDRESSEE: Gen-Probe Incorporated
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Matches 10; Conservative
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           APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDDO, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
TITLE OF INVENTION: STEAROTHERMOPHILUS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                     432 LAQNINITRKE 442
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APPLICATION NUMBER: 08/222,612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-546-7929
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                                                                                                                                                            Application US/09135642
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Pred. No. 0.049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                    APPLICANT: RIGGS, MICHAEL G. APPLICANT: SIVARAM, MATHOOR APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
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HYPOTHETICAL:
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CURRENT APPLICATION DATA:
                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                               432 LAQNINITRKE 442
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                               COMPUTER:
                                                                                          COUNTRY:
                                                                                                           STATE:
                                                                                                                        ADDRESSEE: Gen-FIGURE STREET: 9880 Campus Point Drive
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REGISTRATION NUMBER: 3
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SOFTWARE:
             OPERATING SYSTEM:
                                                                             ZIP:
                                                                                                                       CITY: San Diego
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FastSEQ Version 1.5
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IBM Compatible
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                                                                                                                                                          Gen-Probe Incorporated
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APPLICANT: HUANG, WEI-HUA

FITTE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE
FITTE OF INVENTION: DYE-LABELED DIDEOXYNDGLEOTIDES
FILE REFERENCE: longsequencelisting
FILE REFERENCE: longsequencelisting
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                                                                                                                                ; ORGANISM: Bacillus stearothermophilus US-09-157-397-2
                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0 - beta
SEQ 1D NO 2
LENGTH: 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09157397 Patent No. 6165765
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                                                                                             Query Match
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                                                                                    Best
                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1998-09-21 EARLIER APPLICATION NUMBER: 08/
                                                                                                                                                                                                                                   NUMBER OF SEQ 1D NOS: 11
                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/642,584 EARLIER FILING DATE: 1996-05-03
                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1995-10-
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/157, 397
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ORIGINAL SOURCE:
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432 LAQNLNITRKE 442
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                                                                                 Local Similarity
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                             1 LAQNLNIXKKE 11
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                                                                 Conservative
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                                                                             Score 48; DB 4;
Pred. No. 0.049;
                                                                 Mismatches
                                                                                             DB 4; Length 587;
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                                                                                                                US-08-436-664-25
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US-09-517-871-22
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Sequence 25, Application US/0843664
Patent No. 5874202
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SIVARAM, MATHOOR
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STRALA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/517,871
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 587
TYPE: PRT
                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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APPLICANT: Gu, Trent
TITLE OF INVENTION: Method of Reverse Transcription
FILE REFERENCE: PRMG-03833
                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hartnett, John R.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 587 amino acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                             432 LAQNLNITRKE 442
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/04080
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34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PURIFIED DNA POLYMERASE FROM BACILLUS
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Pred. No. 0.049;
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US-09-135-642-25
; Sequence 25, Applica
; Sequence 6066483
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                                  CITY:
STATE:
   COUNTRY: UZIP: 92121
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                                                                STREET:
                                                                             ADDRESSEE:
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                   APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
TITLE OF INVENTION: PURIFED
TITLE OF INVENTION: STEAROTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                             433 LAQNLNITRKE 443
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CITY: San Diego
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              San Diego
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                                                                                                                                                                                                                                        Application US/09135642
                                             E: Gen-Probe Incorporated 9880 Campus Point Drive
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USA
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                                                                                                                   TUDOR, STARLA D.
VENTION: PURIFED DNA POLYMERASE FROM BACILLUS
VENTION: STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 0.049;
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US-08-394-232A-25
US-08-394-232A-25
; Sequence 25, Application US/08394232A
; Patent No. 6100078
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Best Local Similarity
Watches 10; Conserve
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; ORIGINAL SOURCE:
US-09-135-642-25
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                               Patent No. 6100078
GENERAL INFORMATION:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICATION NUMBER: 08/307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
APPLICATION NUMBER: 08/222,612
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                                                            SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                             APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPL: Diskette
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                                                                                                                                                                COUNTRY:
                                                                                                               COMPUTER:
                               FILING DATE:
                                             APPLICATION NUMBER: US/08/394,232A
                                                                                             OPERATING SYSTEM:
                                                                                                                           MEDIUM TYPE:
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TELEFAX: 619-546-7929
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                                                                                                                                                                                                           San Diego
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                                                                                            PE: Diskette
IBM Compatible
SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 3; Length 588; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                          뮹
                                      Search completed: January 15, 2003, 12:38:26 Job time: 10.2857 secs
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                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                          10;
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; SOFTWARE: Patentln Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-157-397-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-394-232A-25
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09157397 Patent No. 6165765
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE TITLE OF INVENTION: SELECTIVE DISCRIMINATION AGAINST FLUORESCENT TITLE OF INVENTION: DYE-LABELED DIDEOXYNUCLEOTIDES FILE REFERENCE: hongsequencelisting CURRENT APPLICATION NUMBER: US/99/157,397 CURRENT APPLICATION NUMBER: US/99/157,397 EARLIER APPLICATION NUMBER: 08/544,643 EARLIER FILING DATE: 1995-10-18 EARLIER FILING DATE: 1995-05-10-18 EARLIER APPLICATION NUMBER: 08/542,684 EARLIER APPLICATION NUMBER: 08/642,684 EARLIER FILING DATE: 1996-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HONG, GUOFAN APPLICANT: HUANG, WEI-HUA
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: P
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 LAQNLNITRKE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GPOILECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fisher, Carlos A REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 619-535-28 TELEFAX: 619-546-7929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/3
FILING DATE: 16-SEP-1994
                                      1 LAQNINIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588 amino acids
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                                                                               Conservative
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90.9%;
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                                                                           Score 48; DB 4; Length 588; Pred. No. 0.049; 0; Mismatches 1; Indels
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                                                                           Gaps
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Result
No.
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-DB=1ssued_Patents_NA -QFMT=fastap -SUFFIX=rn1 -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MAGRIX-blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9823649_eCGN_1_1_35_@runat_14012003_151002_29127 -NCPU=6 -ICPU=3
-NO_KIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LOORGCO -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  Score
     44444444448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-823-649A-7
49
1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    January 15, 2003, 12:36:21; Search time 26 Seconds (without alignments) 129.748 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
                                                                                                                                                                                                                                Length DB
   1142
1379
1625
1764
1764
1764
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1764
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US-09-057-969-12

US-09-057-969-11

US-09-057-969-10

US-09-057-969-9

US-08-642-684-1

US-08-436-646-22

US-08-394-232A-22

US-09-157-397-1

US-09-157-397-3

US-09-157-397-3

US-09-517-871-21

US-09-517-871-21

US-09-517-871-21
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7.0
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                               Sequence
                                                                                                                                                                                                                              Description
                             12, Appl
11, Appl
10, Appl
10, Appli
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12, Appl
122, Appl
122, Appl
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122, Appl
122, Appl
123, Appli
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US-09-057-969-12
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; Patent No. 6013451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                  STATE:
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45	44	43	42	41	40	9	38	37	36	S	34	S S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	8	17	16	15	14	13
48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	4.8	40	48	48	48	48	48	4.8	48	48	48	48	48	48	48	48
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76	76	53	63	63	2631	2631	2631	2631	2631	2631	2631	2631	2631	2631	2631	2631	2631	2631	1880	1779	1779	1779	1773	1773	1773	1773	1770	1767	1767	1767	1767	1767
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-09-135-642	08-436-664-19	<b>S</b> 95-04080-	-US95-04080-3	-US95-04080-2	9-517-87	-09-517-871-1	-394-232A-3	-08-394-232A-3	94-232A-	-135-642-3	-09-135-642-3	9-135-642-2	-436-664-3	-08-436-664-3	6-664	-08-510-215	8-428-823	-08-208-036-1	-09-057-969	9-517-871	8-823	8-208-036-16	US95-04080-	8-394-232A-2	-09-135-642-2	-08-436-664-2	8-642-684-3	r-us95-04080	-09-517-871-5	08-394-232A	-09-135-642-2	64 -
Sequence 19, Appl	19, App	33, App	31, App	21, App	19	1, Appl	, App	<u>ω</u>	Sequence 21, Appl	33, App	31, App	21.	33, App	App	21, App	1, Appl	13, App		8, Appl	3, Appl	Sequence 16, Appl	16				26, App	3. Appl	24	5. Appl	24. App		

## ALIGNMENTS

TAN, TIEN CHYE PHANG, WONG,

VICTOR THI WONG

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INFORMATION FOR SEQ ID NO:
                                    CLASSIFICATION: 435
ATTORNAY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 6745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 101
                      TELEFAX:
                                                                                                                                                                          APPLICATION NUMBER: US/09/057,969 FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                   3: FROMMER LAWRENCE & HAUG LLP
745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                               USA
                        212-588-0500
                                                                                                                                                        09-APR-1998
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS STEAROTHERMAPHILUS DNA
POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED
3'-TO-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
    12
                                                                            674507-2001
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Percent Similarity:
Best Local Similarity:
                                                                                                                                         ; MOLECULE TYPE: US-09-057-969-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-09-057-969-12
                                                                                        Pred. No.:
                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-057-969-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-823-649A-7 (1-11) x US-09-057-969-12 (1-890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Appli
Patent No. 6013451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                            TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PHANG, SENG MENG
APPLICANT: TAN, TIEN CHYE
TITLE OF INVENTION: BACILUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENCW) CLONES INCLUDING THOSE REDUCED TO
TITLE OF INVENTION: 33-T0-5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WONG, VICTOR THI WONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 357
                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 NAME: KOWALSKI, THOMAS J. REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 679
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/057,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                             H: 1142 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998
N: 435
                                                                                                                                                          DNA (genomic)
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48.00
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90.91%
97.96%
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   Indels:
Gaps:
                                      Mismatches:
                                                    Conservative:
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                                               GENERAL INFORMATION:
            APPLICANT: APPLICANT:
APPLICANT:
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Percent Similarity:
Best Local Similarity:
Query Match:
US-09-057-969-9
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                                                                                                                 US-09-823-649A-7 (1-11) x US-09-057-969-10 (1-1379)
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                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 212-580-000 10:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: /**
CITY: NEW YORK
CTATE: NEW YORK
TISA
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APPLICANT: PEANG, SENG MENG
APPLICANT: TAN, "1 EN CHYE
TITLE OF INVENTION: BACILLUS STEAROTHERMAPHILUS DNA
TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
NUMBER OF EQUUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                           577 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 609
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                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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09-APR-1998
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WONG, VICTOR THI WONG PHANG, SENG MENG TAN, TIEN CHYE

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US-08-642-684-1
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                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08642684 Patent No. 5834253
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                 APPLICANT: FENG, ZHAI
APPLICANT: HUANG, WEI-HUA
TITLE OF INVENTION: 3'_5' EXONUCLEASE WITH PROOF-READING
TITLE OF INVENTION: 3'_5' EXONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 674507-2001
TELECOMMUNICATION INFORMATION:
                                                                      COMPUTER READABLE FORM:
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LENGTH: 1625 base pairs
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polomine
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                                                                                                            COUNTRY:
                                                                                                                              STATE:
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                                                                                                                                               WASHINGTON
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745 FIFTH AVENUE
                                                                                                                                                            1100 NEW YORK AVENUE, N.W.
                                                                                                             USA
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                                                                                                                                                                                                                                                                                                      HONG, GUO FAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
       PatentIn Release #1.0, Version #1.25
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POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO
3'-TO-5' EXONUCLEASE ACTIVITY
17
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Patent No. 50,...
RIGGS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                       FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: "UDDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                               CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                      FILING DATE:
APPLICATION NUMBER:
FILING DATE: 16-SEE
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                  NAME: Fisher, Carlos A REGISTRATION NUMBER: 3
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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STRANDEDNESS: single
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                                                                                         APPLICATION NUMBER: 08/222,612
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                    SOFTWARE:
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   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                                                                                                                                           9880 Campus Point Drive
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                    36,510
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Indels:
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Pred.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6066483
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22,
                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1764 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS TITLE OF INVENTION: STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                               STATE:
            NAME: Fisher, Carlos A REGISTRATION NUMBER: 3
                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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REFERENCE/DOCKET NUMBER: GP94003.CP2
                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive
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            36,510
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US-08-394-232A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KIGGS, MICHAEL C.
APPLICANT: SIVARAM, MATHOUR
APPLICANT: TUDOR, STARLA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                              APPLICATION NUMBER: 08/222,612
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: GP9400
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/31
FILING DATE: 16-SEP-1994
              TELEPHONE: 619-535-2807
                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILU NUMBER OF SECUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
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                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/394,232A
                                                                                                                                                                                                                                                                               SOFTWARE:
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US-09-157-397-3
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; ORGANISM: Bacillus stearothermophilus
US-09-157-397-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HONG, GUDFAN
APPLICANT: HONG, WEI-HUA
APPLICANT: HONG, WEI-HUA
TITLE OF INVENTION: SELECTIVE DISCRIMINATION AGAINST FLUORESCENT
TITLE OF INVENTION: DYE-LABELED DIDEOXYNUCLEOTIDES
FILE REFERENCE: hongsequencelisting
CURRENT APPLICATION NUMBER: US/09/157,397
CURRENT APPLICATION NUMBER: US/09/157,397
CURRENT FILING DATE: 1998-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/544,643
EARLIER FILING DATE: 1995-10-18
EARLIER APPLICATION NUMBER: 08/642,684
EARLIER FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09157397 Patent No. 6165765
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 - beta
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                                                   1294 TIGGCGCAAAACTIGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1764
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                                                                                    1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
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Conservative:
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PCT-US95-04080-22
                                                                                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bacillus stearothermophilus US-09-517-871-21
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Best Local Similarity:
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US-09-157-397-3
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; LENGTH: 1764
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; Patent No. 643667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hartnett, John R.
APPLICANT: Huang, Fen
APPLICANT: Gu, Trent
TITLE OF INVENTION: Method of Reverse Transcription
FILE REFERENCE: PRMG-03833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/642,684
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0 - beta
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                                                 1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
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No.:
                                                                                  1 LeuAlaGinAsnLeuAsnIle***ArgLysGlu 11
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Matches:
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US-09-823-649A-7 (1-11) x PCT-US95-04080-22 (1-1764)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1294 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PURIFED DNA POLYMER TITLE OF INVENTION: STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          COUNTRY: US
ZIP: 92121
FILING DATE:
                            FILING DATE:
                                               APPLICATION NUMBER:
                                                                                            APPLICATION NUMBER: FILING DATE: 08-MA
                                                                                                                                                         OPERATING SYSTEM:
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               CATION NUMBER:
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                                                                                                                                                                                                                                                                                       E: Gen-Probe Incorporated 9880 Campus Point Drive
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                                                                                                                                                                                                                                                                                                                                                                                       SIVARAM, MATHOOR TUDOR, STARLA D.
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                                                                                                                                                                       IBM Compatible
                                                                                        08-MAY-1995
                                                                                                                                                                                        Diskette
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               08/307,410
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                                              08/394,232
                                                                                                           US/08/436,664
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Indels:
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RESULT 14
US-09-135-642-24
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Sequence 24, Applic
5 - Applic
5 - Applic
6066483
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APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVAKAM, MATHOOR
APPLICANT: TUDOK, STAKLA D.
TITLE OF INVENTION: PURIFFED DNA POLYMERASE FROM BACILLUS
TITLE OF INVENTION: STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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FILING DATE: 16-SEP-199%
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A
NAME: Fisher, 36,
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LENGTH: 1767 base pairs
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OTHER INFORMATION:
APPLICATION NUMBER: 08/3 FILING DATE: 16-SEP-1994
                                                                                 CLASSIFICATION:
                                                                                                   FILING DATE:
                                                                                                               APPLICATION NUMBER: US/09/135,642
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                               ADDRESSEE: Gen-Probe Incorporated STREET: 9880 Campus Point Drive
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                                  FILING DATE:
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                                                                                                                                                                                                                                                                                 San Diego
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-394-232A-24
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SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
                             PRIOR APPLICATION NUMBER: 8,307,410
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: 08/222,612
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: RIGGS, MICHAEL G.
APPLICANT: SIVARAM, MATHOOR
APPLICANT: TUDOR, STARLA D.
TITLE OF INVENTION: PURIFED DNA POLYMERASE FROM BACHILUS STEAROTHERMOPHILU
                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
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                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                      ZIP:
                 FILING DATE:
                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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CITY: San Diego
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                                                                                                                                    APPLICATION NUMBER: US/08/394,232A
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Search completed: January 15, 2003, 12:58:58 Job time: 30 secs
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                                                                                                                                                 Query Match:
                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                US-08-394-232A-24
                                                                                                                                                                                           Score:
                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
                                                   1297 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1329
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CH
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                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 1...1764
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1767 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                             OTHER INFORMATION:
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                                                                  1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
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Minimum DB seq length: 0
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Maximum Match 100%
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                               /SIDS2/gcgdata/geneseq/genesegn-embl/NA2002.DAT:*
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                                                                                                                                                                                                                                                                                                   AAT36360 standard; DNA; 1763 BP
                                         EP757100-A1
                                                                           Bacillus stearothermophilus
                                                                                                                                        DNA polymerase;
                                                                                                                                                                            Bst DNA polymerase large fragment DNA.
                                                                                                               polymerase; Bst Pol I; thermostable enzyme; exonuc sequencing; strand displacement amplification; ss.
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AAT78171
AAT78170
AAX13058
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ABL17784
ABL17768
AAS89981
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AAT97089
ABL26758
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Bacillus lichenifo
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RESULT 2
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DB:
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                                     24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA construct (AAT36360) codes for Bacillus stearothermophilus (Bst) DN1 polymerase large iragment (AAW10597) which lacks the N-terminal 3'-5' exonuclease domain of the native enzyme. It comprises nucleotides 868-2631 of the full-length Bst polymerase coding sequence, and was obto by PCR cloning (see also AAT60826-27) using Bst genomic DNA as template. The DNA construct can be used to produce recombinant Bst polymerase large fragment, pref. as a fusion protein with maltose binding protein, in Lransformed host cells. The product can be used for nucleic acid sequencing and strand displacement amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding recombinant thermophilic Bacillus stearothermophilus DNA polymerase I - substantially free of 3'-5', and opt. also 5'-3' exonuclease activity
                                                                                          30-MAR-1995;
                                                                                                                                              W09527067-A1
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                   sequencing;
                                                                                                                                                                                                                 amplification;
                                                                                                                                                                                                                              Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer;
                                                                                                                                                                                                                                                        B.stearothermophilus DNA polymerase clone Bst2.
                                                                                                                                                                                                                                                                                   30-MAY-1996
                                                                                                                                                                                                                                                                                                              AAT04802;
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           (GENP-) GEN-PROBE INC
                                                                                                                    12-OCT-1995
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                                                                                                                                                                                                 on; probe; Bacillus caldotenax; exonuclease; recombination; polymerase chain reaction; ss.
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                                   95US-0394232.
94US-0222612.
94US-0307410.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of the clone Bst2 encoding a modified Bacillus stearothermophilus thermostable DNA polymerase which lacks the complete 5'-3' exonuclease domain. The gene was constructed by ligating the HindIII-SalI fragment from the clone pdemBst2.1Sst contg. 3' end of the gene with the Sty1-HindIII fragment of the clone pdemBst5'end contg. the 5' end of the DNA polymerase gene. The Sty1-HindIII fragment covers the mid-region of the gene up to and including the sequences encoding the 3'-5' exonuclease but not the 5'-3' exonuclease domain. The remainder of the 5' end of the gene was reconstituted by the ligated and extended oligonucleotides AATO4816-17. The modified DNA polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
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                                                                                                                                       03~MAY-1996;
18-OCT-1995;
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                                                                                                                                                                                                                                                                            26-AUG-1997.
                                                                                                                                                                                                                                                                                                                                JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA replication; exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus; DNA polymerase; DNA amplilication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-373510/48.
P-PSDB; AAR81039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                (HONG/)
                                                         (NAUH)
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                                                                                HONG G F.
                                                      HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stearothermophilus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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95US-0544643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 A; 456 C;
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase. This heat stable DNA polymerase has a peptide sequence of 587 amino acids. This DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of
Claim 8; Page 93-95; 109pp; English
                                                                                      WPI; 2000-283563/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
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                                    New DNA polymerase, useful all four dideoxynucleotide
                                                                          P-PSDB; AAY91930.
                                                                                                                Hong G,
                                                                                                                                                                                                                                                                                                                                                B. stearothermophilus 320 modified DNA polymerase coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the DNA sequence of the Bacillus stearothermophilus strain DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt DNA} polymerase from Bacillus stearothermophilus - used in {\tt DNA} amplification and sequencing methods having lower frequency of
                                                                                                                                           (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE
                                                                                                                                                                   21-SEP-1998;
                                                                                                                                                                                            14-JAN-1999;
                                                                                                                                                                                                                       30-MAR-2000
                                                                                                                                                                                                                                              WO200017330-A1
                                                                                                                                                                                                                                                                       Bacillus
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                         Modified DNA polymerase; DNA sequencing; 3' to 5' exonuclease activity; random primer labeling; site-directed mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA clone can be avoided.
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                                                                                                              Huang W;
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                                    particularly in DNA sequencing, inco-
triphosphate terminators with about
                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a modified Bacillus stearothermophilus DNA polymerase (AAY91930) that, during DNA sequencing, effectively incorporates all four fluorescent dye-labeled dideoxynucleotide triphosphates (ddN"P), or their analogs, and reduces the discrimination, observed with the unmodified enzyme, for incorporation of labeled dCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exounclease activity during DNA sequencing from a template and the polymerase excises mismatched nucleotides from the 3' torminus at a faster rate than it removes correctly matched nucleotides. The polymerase is used particularly for DNA sequencing, also for filling in
                                                                                                                                                                                                                                                                                                                                    New DNA polymerase, useful all four dideoxynucleotide
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                                                                                                                                                                                                                                                                                                   efficiency
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دو
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase; DNA sequencing; 3' to 5' exonuclease act r labeling; site-directed mutagenesis; wild type; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Σ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
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The present sequence encodes a wild type Bacillus Stearothermophilus DNA polymerase (AAY91931) that is modified (see AAY91930) so that during DNA sequencing, it effectively incorporates all four fluorescent dye-labeled dideoxynucleotide triphosphates (ddNTP), or their analogs, and reduces the discrimination, observed with the unmodified enzyme, for incorporation of labeled ddCTP and ddATP, is new. The modified DNA polymerase, has proofreading 3'-5' exonuclease activity during DNA

Example 2; Page 80-82; 109pp; English.

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RESULT 6
AAD18459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity:
The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing from a template and the polymerase excises mismatched nuclectides from the 3' terminus at a faster rate than it removes correctly matched nuclectides. The polymerase is used particularly DNA sequencing, also for filling in 5' overhangs, synthesis of DNA
                                                                                                                                                                              Reverse transcription of RNA using Two and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000; 2000US-0517871
                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD18459 standard; DNA; 1764
                                                                                                                             Claim 9; Fig 9; 118pp; English.
                                                                                                                                                                                                                                                          P-PSDB; AAE11060
                                                                                                                                                                                                                                                                                                                                                   (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001; 2001WO-US06571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bst; enzyme; amplification; hybridisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus (Bst) DNA polymerase 1 fragment DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1764 BP; 477 A; 415 C; 486 G; 386 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuAlaGlnAsnLeuAsnTle***ArgLysGlu 11
                                                                                                                                                                                                                                                                               2001-589872/66.
                                                                                                                                                                                                                                                                                                               Huang F, Hartnett JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by random primer labeling and in site-directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Bacillus stearothermophilus DNA polymerase ]"
/note= "CDS does not include start codes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-823-649A-7 (1-11) x AAD18459 (1-1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation of target DNA, hybridisation of primers and synthesis of complementary strands. The present DNA sequence is Bacillus stearothermophilus (Bst) DNA polymerase 1 fragment which lacks 5' to 3' exonuclease activity.
                          digestion and recombination of the full length gene (AAT04801) to remove a 195 bp Hincil-evull fragment from the region encoding the 5'-3' exonuclease. The deleted fragment removes 65 amino acids (residucs 178-242 of the protein) including 2 Gly residues though to correspond to 2 amino acids in the E.coli DNA polymerase I necessary for 5'-3' exonuclease activity. The modified DNA polymerase can be used in primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1294 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1326
                                                                                                                                          This is the nucleotide sequence of the clone Bst3 encoding a modified Bacillus stearothermophilus thermostable DNA polymerase which contains a Bacillus stearothermophilus thermostable DNA polymerase which contains a Bacillus tearothermophilus thermostable DNA polymerase which contains a Bacillus in the 5'-3' exonuclease domain. The gene was constructed by
                                                                                                                                                                                                                         Claim 9; Page 87-90; 135pp; English.
                                                                                                                                                                                                                                                                                                                                           WP1; 1995-373510/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplification; probe; Bacillus caldotenax; exonuclease; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.stearothermophilus DNA polymerase clone Bst3
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                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus DNA encoding thermostable polymerase -
                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR80140.
                                                                                                                                                                                                                                                                                                                                                                                                                      (GENP-) GEN-PROBE INC
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                                                                                                                                                                                                                                                               for nucleic acid sequencing and amplification
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extension reactions such as DNA sequencing or polymerase chain reaction

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            thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Bacillus stearothermophilus (Bst) DNA polymerase. Tvu and Bst DNA polymerase are useful for reverse transcription reactions which allows repetitive heating/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR wherein reverse transcription and amplification are performed in a single continuous procedure. Primers, template, nucleoside triphosphates, appropriate reaction buffer having magnesium ions, reaction conditions, and polymerase are used in the PCR process, which involves denaturation
                                                                                                                                                                                                                                                                                          Reverse transcription of RNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                                                                         c
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                                                                                                                                                                                           The invention relates to reverse transcription of RNA templates using
                                                                                                                                                                                                                                     Example 11; Fig 5; 118pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reverse transcription; DNA polymerase; Thermoactinomyces vulgaris; Tvu
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                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hartnett JR;
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Indels:
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having DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Twu DNA polymerase can be used for processes of high temperature nucleic acid amplification and sequencing without substantial loss of DNA synthesis activity. The enternal because transcription in the
                                                                                                   The invention provides compositions comprising thermostable DNA polymerases derived from hyperthermophilic eubacteria, in particular, a purified and isolated Thermoactinomyces vulgaris (Tvu) DNA polymerase
                                                                                                                                                                                     Claim 17; Fig 7; 113pp; English.
                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                       Gu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000US-0517439
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                                                                                                                                                                                                                                                                                                                                                                                                              (PROM-) PROMECA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001; 2001WO-US06436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deletion mutant; T289M; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tvu DNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                    Huang
                                                                                                                                                                                                                                                                                                             AAB85951
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                                                                                                                                                                                                                                                                                                                                                                       |T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*Lag-
                                                                                                                                                                                                                                                                                                                                                                       Hartnett
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US-09-823-649A-7 (1-11) x AAD18445
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Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including amplification, reverse transcription and sequencing reactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable; DNA polymerase; hyperthermophilic; DNA synthesis;
Tvu DNA polymerase; nucleic acid amplification; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuAlaGlnAsnLeuAsnIle***ArgLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Tvu DNA polymerase M285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deletion mutant T289M encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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RESULT 10
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ID AAT90
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This DNA sequence of the Bacillus stearothermophilus strain encodes a heat stable DNA polymerase. This DNA polymerase has a peptide sequence of 589 amino acids. This DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             absence of manganese ions and in high throughput robotically-manipulated procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary structure is removed or limited. The present sequence represents the nucleotide sequence encoding a 5′-3′ exonuclease deletion mutant form of Tvu DNA polymerase called T289M.
                                                                                  Claim 13; Pages 27-28; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                     JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus stearothermophilus; DNA polymerase; DNA replication; exonuclease; proof reading;
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                                                                                                               mismatch
                                                                                                                                                                                WPI; 1997-474304/44
                                                                                                                                                                                                                                                                                                       03-MAY-1996;
18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. stearothermophilus. PNA polymerase encoding full length DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT90820 standard;
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                                                                                                                       DNA polymerase from Bacillus stearothermophilus - used in DNA amplification and sequencing methods having lower frequency of
                                                                                                                                                                    P-PSDB; AAW30094.
                                                                                                                                                                                                         Hong GF,
                                                                                                                                                                                                                                                  (ZHAI/)
                                                                                                                                                                                                                                                             (HUAN/)
                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus.
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                                                                                                                                                                                                                                     SHAN-)
                                                                                                                                                                                                                                                                             (HONG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAlaGlnAsnLeuAsnIle***ArgLysGlu
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                                                                                                                                                                                                                                                                            HONG G F.
                                                                                                                                                                                                                                     SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                  ZHAI F.
                                                                                                                                                                                                                                                                HUANG
                                                                                                                                                                                                         Huang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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95US-0544643,
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Conservative:
Mismatches:
Indels:
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                              This is the nucleotide sequence of the clone Bst4 encoding a modified Bacillus Stearothermophilus thermostable DNA polymerase. This clone encodes the sequence of a natural degradation product obtained when the DNA polymerase clone Bst3 (AAT04803) is expressed in E.coli. The same sequence is found when the full length clone (AAT04801) is expressed and cleaved with subtlisin to produce a "Klenow-type" DNA polymerase. This sequence starts with the Val residue at pos. 287 of the full length protein. This contrasts with a commercially available B stearothermophilus DNA polymerase subtlisin fragment where the protein sequence starts with the Ala residue corresp. to pos. 290. The modified DNA polymerase can be used in primer extension reactions such a NA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1300 TTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proof reading 3^{\prime}-5^{\prime} exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination; sequencing; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.stearothermophilus DNA polymerase clone Bst4.
                                                                                                                                                                                                         Claim 9;
                                                                                                                                                                                                                                                Bacillus
                                                                                                                                                                                                                                                                          P-PSDB; AAR80141
                                                                                                                                                                                                                                                                                                                  Riggs MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                   for nucleic
                                                                                                                                                                                                                                                                                                                                            (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09527067-A1
                        sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAlaGlnAsnLeuAsnIle***ArgLysGlu
                                                                                                                                                                                                                                                                                       1995-373510/48.
                                                                                                                                                                                                                               stearothermophilus eic acid sequencing
                                                                                                                                                                                                    Page 92-94; 135pp; English.
                                                                                                                                                                                                                                                                                                                  Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                      95US-0394232.
94US-0222612.
94US-0307410.
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                                                                                                                                                                                                                                                                                                                   Tudor
                                                                                                                                                                                                                               {\tt DNA} encoding thermostable polymerase and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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                                                                                                                                                                                                                                                                                                                  SD;
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Sequence 1773 BP; 433 A; 460 C; 535 G; 345 T; 0 other;

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RESULT 12
AAQ31651
ID AAQ31
Alignment Scores:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                  03-JUN-1991;
07-NOV-1991;
24-FEB-1992;
25-FEB-1992;
06-APR-1992;
                                                          A gene coding for DNA polymerase I was isolated from B.caldotenax YT-G genomic DNA (see AAQ31650). A series of N-terminal deletions was prepared to eliminate the region responsible for 5' to 3' exonuclease activity. Plasmid pUI205 was one of the deletion plasmids which still expressed PolI activity but for which no 5' to 3' exonuclease activity was detected. The insert contained in pUI205 is identical to nucleotides 1900 to 2868 of AAQ31650. E.coli HB101 transformed with pUI205 produced a heat-resistant DNA polymerase of mol. wt. 67,000 by SDS-PAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1303 CTGGCGCAAAACTTGAACATTACGCGCAAAGAA 1335
                         Sequence 1779 BP;
                                                                                                                                                                                            Claim 2; Page 23-24; 30pp; English.
                                                                                                                                                                                                                  Gene for PolI type DNA polymerase and cloning method - production of DNA polymerase in high yield.
                                                                                                                                                                                                                                                            P-PSDB; AAR28349
                                                                                                                                                                                                                                                                        WPI; 1992-408872/50.
                                                                                                                                                                                                                                                                                                 Fujita K, Ishino Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP517418-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus caldotenax truncated DNA PolI gene in plasmid pUI205.
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                                                                                                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ31651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A polymerase; polymerase chain reaction; strain YT-G; DSM406 to 3' exonuclease activity; ds.
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                                                  AAR28340-R28347 and AAQ31648-Q31649
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                                                                                                                                                                                                                                                                                                                                                  91JP-0318685.
92JP-0072090.
92JP-0073161.
92JP-0112400.
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1..1779
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/product% N-terminally_deleted_Poll
/note= "5'to 3' exonuclease activity deleted"
                         446 A; 425 C; 529 G; 379 T; 0 other;
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The invention relates to reverse transcription of RNA templates using thermostable DNA polymerase such as Thermoactinomyces vulgaris (Tvu) and Each DNA polymerase. Tvu and Est DNA CC polymerase are useful for reverse transcription reactions which allows CC repetitive healing/cooling cycles without the requirement of fresh enzyme at each cooling step. The invention contemplates single-reaction RT-PCR CC wherein reverse transcription and amplification are performed in a single CC continuous procedure. Primers, template, nucleoside triphosphates, CC appropriate reaction buffer having magnesium ions, reaction conditions, CC and polymerase are used in the PCR process, which involves denaturation CC of target DNA, hybridisation of primers and synthesis of complementary CC strands. The present sequence is Thermoactinomyces vulgaris (Tvu) DNA CC polymerase M285 truncated mutant DNA. This Tvu M285 mutant DNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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                                                                                                                                                                                                                                                                                        Reverse transcription of kNA using Tvu and Bst DNA polymerase, comprises combining the polymerase, RNA containing sample, a primer and reaction buffer having magnesium ions and reacting the mixture to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                                                                                                                                                                                                                                 Example 11; Fig 3; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000; 2000US-0517871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse transcription; DNA polymerase; Thermos enzyme; amplification; hybridisation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoactinomyces vulgaris DNA polymerase M285 truncated mutant DNA.
                                                                                                                                                                                                                                                                                   obtain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                         2001-589872/65.
                                                                                                                                                                                                                                                                                                                                                                                                       Huang F,
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/product= "Thermoactinomyces vulgaris DNA polymerase
//285 truncated mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Best Local Similarity:
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                                                                                      having DNA synthesis activity. It is useful for determining the nucleotide base sequence of a DNA molecule. Two DNA polymerase can be used for processes of high temperature nucleic acid amplification and sequencing without substantial loss of DNA synthesis activity. The enzyme can be used to perform high temperature reverse transcription in the absence of manganese ions and in high throughput robotically manipulated
                               procedures because greater enzymatic stability is retained at room temperature. Using the Tvu DNA polymerase, reverse transcription reactions can be conducted at increased temperatures so that secondary structure is removed or limited. The present sequence represents the
                                                                                                                                                                             The invention provides compositions comprising thermostable DNA polymerases derived from hyperthermophilic eubacteria, in particular, polymerases a purified and isolated Thermoactinomyces vulgaris (Yvu) DNA polymerase
   nucleotide sequence encoding a 5'-3' Tvu DNA polymerase called M285.
                                                                                                                                                                                                                                                                                      Novel thermostable DNA polymerase derived from Thermoactinomyces vulgaris for us in many recombinant DNA techniques, including
                                                                                                                                                                                                                                           Claim 17; Fig 5; 113pp; English
                                                                                                                                                                                                                                                                         amplification, reverse transcription and sequencing reactions
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/product= "Tvu DNA polymerase M285"
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                                                          Sequence 2631
                                                                                                                                                                                                                                                                                      Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                           Riggs MG,
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01-APR-1994;
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                                                                                                                                                                                                                                                                                                               for nucleic acid sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENP-) GEN-PROBE INC
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                                                                                                                                                                                                                                                                                                                                                                                                           Sivaram M,
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94US-0222612.
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US-09-823-649A-7 (1-11) x AAH47392 (1-1779)
                                                    This is the sequence of the coding region of the gene encoding the Bacillus stearothermophilus thermostable DNA polymerase. The gene was isolated using the PCR primers and probes AAT04807-15 which were based on sequence similarity with the Bacillus caldotenax DNA polymerase gene. The gene was isolated as two overlapping fragments of 885 and 1143 bp corresp. to the 3' end and the 3'-5' exonuclease region of the protein, resp. Those amplification fragments were used to probe Southern gels and isolate the 3' and 5' ends of the gene as two separate fragments. The complete gene (AAT04801) was subsequently polymerase can be used in primer extension reactions such as DNA sequencing or polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus DNA encoding thermostable polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 79-82; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compug
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                              US-08-484-956-90
US-08-527-653-90
US-08-527-653-90
US-09-096-399-2
US-09-096-399-4
PCT-US95-14418-5
PCT-US95-14418-5
PCT-US95-14418-5
PCT-US95-15327-4
US-09-787-538-2
US-09-787-538-2
US-09-787-538-2
US-09-787-636-20-4
US-08-156-020-4
US-08-156-020-10
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(without alignments)
34.855 Million cell updates/sec
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US-08-484-956-90
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                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 09-MAR-19
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: US
FILING DATE: 09-NOV-19
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION OBTA:
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TITLE OF INVENTION: D
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
COMPUTER: IBM PC componenting SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Paleutin Rel
CURRENT APPLICATION DATA:
                                                         FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARRPOLL ], PETER G.
REGISTRATION NUMBER: 32,83
                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 22
CITY: SAN
STATE: CAL
COUNTRY: U
                                           REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
               TELEPHONE:
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220 MONTGOMERY
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(415) 397-8338
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LYAMICHEV, VICTOR I.
BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                PaleutIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                               B: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               NUMBER: US 08/254,359
06-JUN-1994
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STREET, SUITE 2200
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US-08-254-359A-8
US-08-483-043-8
US-08-481-238-8
US-08-471-0668-8
US-08-464-956-8
US-08-484-956-8
US-08-757-653-8
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US-08-756-386-4
US-08-82-516-4
US-08-682-853A-4
US-08-759-038-4
US-08-759-038-4
US-09-350-309-4
US-08-978-946-4
US-08-978-986-2
PCT-US91-07035-2
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RESULT 3
US-08-520-946-90
; Sequence 90, Application US/08520946
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-757-653-90
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US-08-757-653-90
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NAME: INGOLIA, Dianc E.
REGISTRATION NUMBER: 40,027
REFERENCE/POCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5843669
GENERAL INFORMATION:
                                                                                                                                                             Matches
                                                                                                                                                                            Query Match 100.0%; Score 54; DB 2; Length 528; Best Local Similarity 100.0%; Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                        374 LSQELAIPYEE 384
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco. *
STATE: California
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                                                                                                                           1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-520-946-90
                                                                                                                                         ; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
   Matches
                                    Query Match
                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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GENERAL INFORMATION:
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APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
                                                                                                                                                                                                                                                                          APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
TTILE OF INVENTION: Thermostable Polymerase
FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Applic Patent No. 6130045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best local Similarity 100.0%;
Matches 11; Conservative
                      Best Local Similarity
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/096,399A
CURRENT FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                     ORGANISM: Artificial Sequence
                                                                                       OTHER INFORMATION: Recombinantly engineered mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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     Conservative
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415) 397-8338
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                 100.0%;
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                 Score 54; DB 4; Length 553; Pred. No. 0.023;
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Pred. No. 0.022;
   Mismatches
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 Indels
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Gaps
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                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-021-623C-6
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                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 559
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                             Sequence 4, Application US/09096399A Patent No. 6130045
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                   CURRENT APPLICATION NUMBER: US/09/096,399A CURRENT FILING DATE: 1998-06-11 NUMBER OF SEQ ID NOS: 4
                                                                                                                                     APPLICANT: Wurst, Helmut
APPLICANT: Qui, Zhi-Hao
TITLE OF INVENTION: Thermostable Polymerase
                                                                                                                        FILE REFERENCE: CLON-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn 1.0, v1.25; EDIX; Wordperfect.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk, 5
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 314/231-5400
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                                                                                                                                                                                                                                                                                                                      400 LSQELAIPYEE 410
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CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Blosser, G. Harley
REGISTRATION NUMBER: 33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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6502697583 MCI
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VENTION: Thermostable DNA polymerase with
VENTION: enhanced thermostability and enhanced length and
VENTION: efficiency of primer extension
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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N: 435
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 Mismatches

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RESULT 8
PCT-US95-15327-5
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                                                                                                                        : Sequence 5, Application PC/TUS9515327
: GENERAL INFORMATION:
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Matches
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                CORRESPONDENCE ADDRESS:
                                                                      TITLE OF INVENTION:
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                                                      NUMBER OF SEQUENCES:
                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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NAME: Gass, David A.
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                                                                                                                                                                                                                            406 LSQELAIPYEE 416
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         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PalentIn Release #1.0, Version #1.25
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ses 11; Conserv
                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/14418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                            1 LSQELAIPYEE 11
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Gass, David A.
Gass, David B.
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   6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
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                     Marshall,
                                                                                                                                                                                                                                                                                                             100.0%; Score 54; DB 5; 100.0%; Pred. No. 0.024;
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                                                                    Biologically Active Fragments
Thermus Flavus DNA Polymerase
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O'Toole, Gerstein, Murray & Borun
ower, 233 South Wacker Drive
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                                                                  DNA Polymerase
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PCT-US95-14418-4
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                                                    INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                        REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                          TELEFAX:
                                                                                                                                                                             NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/14418
                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: SOFTWARE: Patenti
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TELEFAX: 312/474-0448
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REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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   POPOLOGY:
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 amino acid
GY: linear
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                                                                                     25-3856
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                                   597 amino acids
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                                                                                                          312/474-0448
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                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Encoding a Thermostable DNA Polymerase Enzyme 51
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Pred. No. 0.024;
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                                                                                                                                                                                           US-09-587-856-2
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                                                                                                                                         GENERAL INFORMATION:
SEQ ID NO 2
                                                                                                                                                          Sequence 2, Application US/09587856 Patent No. 6214557
           CURRENT APPLICATION NUMBER: US/09/587,856
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 9
SOPTWARR: Patentin ver: 2.1
                                                                                   APPLICANT: Washington University
TITLE OF INVENTION: COLD SENSITIVE MUTANT DNA POLYMERASES
FILE REFERENCE: WSHU 2009
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                443 LSQELAIPYEE 453
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Matches

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TELEPHONE: 312/474-6300
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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                   Score 54; DB 5; Length 597, Pred. No. 0.025;
 Mismatches
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US-09-777-537-2
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SEQ ID NO 2
LENGTH: 810
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LENGTH: 810
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                                                              Query Match
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APPLICANT: Kermekchiev, Milko B
TITLE OF INVENTION: COLD SENSITIVE MUTANT DNA POLYMERASES AND METHODS
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: WSHU 2009.2
                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-06 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/777,538
CURRENT FILING DATE: 2001-02-06
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/777,537
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 09/587,856
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APPLICANT: Kermekchiev, Milko B
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                                                                                                                  ORGANISM: Thermus aquaticus
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                                                                                                                                      TYPE: PRT
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TYPE: PRT
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                                Conservative
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                                              Score 54;
Pred. No. (
                                Mismatches
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US-07-977-434-2
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Sequence 2, Application US/07977434 Patent No. 5466591
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                      FILING DATE: 24-JUL-1990 ATTORNEY/AGENT INFORMATION:
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APPLICANT: Abramson, Richard
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
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                                                                                                                         APPLICATION NUMBER: US 557,517
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// FIND TION: 5' TO 3' EXONUCLEASE MUTATIONS OF
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                                                                                                                                                              02-NOV-1990
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15-AUG-1991
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20-SEP-1990
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-156-020-2
Search completed: January 15, 2003, 12:38:22 Job time: 9.28571 secs
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US-08-156-020-2
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
AUTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5474920
GENERAL INFORMATION:
APPLICANT: MOSES M.D., Robb E.
TITLE OF INVENTION: Modified Thermo-Resistant DNA
TITLE OF INVENTION: Polymerases
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION WISER: US/08/156,020
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                 1 LSQELAIPYEE 11
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678 LSQELAIPYEE 688
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CITY: Chicago
STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Allegretti & Witcoff STREET: 10 South Wacker Drive
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                                                                                                                                                                     100.0%; Score 54; DB 1; Length 832; illarity 100.0%; Pred. No. 0.037; Conservative 0; Mismatches 0; Indels
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Database :
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                               Score
        protein search, using sw model
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : /cgn2_6//ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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2: /cgn2_6//ptodata/2/pubpaa/US10_NEW_PUBCOMB.pep:*
3: /cgn2_6//ptodata/2/pubpaa/US10_PUBCOMB.pep:*
4: /cgn2_6//ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-823-649A-10

US-09-823-649A-11

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US-09-823-649A-13

US-09-823-649A-13

US-09-823-649A-13

US-09-823-649A-13

US-10-93-297-4

US-10-91-805-1

US-10-93-297-6

US-10-033-297-6

US-10-033-297-71

US-10-031-806-6

US-10-031-806-6

US-10-9777-430A-11
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Sequence 3, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                             Description
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GENERAL INFORMATION:

APPLICANT: Smith, Edward

APPLICANT: Elistrom, Carita

APPLICANT: Gelfand, David

APPLICANT: Higuchi, Russell

APPLICANT: Myers, Thomas

US-09-823-649A-3

Sequence 3, Application US/09823649A Patent No. US20020012970A1

## ALIGNMENTS

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RESULT 2
US-09-823-649A-8
: Sequence 8, Application US/09823649A
: Patent No. US20020012970A1
: GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                         y Match 100.0%; Score 54; DB 10; Local Similarity 100.0%; Pred. No. 0.00018; hes 11; Conservative 0; Mismatches 0;
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                                                                                                                                               LSQELAIPYEE 11
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RESULT 4
US-09-823-649A-11
Sequence 11, Application US/09823649A
Featent No. US20020012970A1
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APPLICANT: Elfstrom, Carj
APPLICANT: Gelfand, Davic
APPLICANT: Higuchi, Russe
APPLICANT: Myers, Thomas
                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ JD NOS: 21
SOFTWARE: PARCEL TO SEE SOFTWARE: PARCEL TO SOFTWAR
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Best Local Similarity
APPLICANT: Smith, Edward
APPLICANT: Elfstrom, Cari
APPLICANT: Gelfand, David
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CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
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APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
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TYPE: PRT
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Myers, Thomas
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Pred. No. 0.00018;
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US-09-823-649A-13
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                                                                                                      Sequence 4, Application US/10033297
Publication No. US20020187486A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09823649A Patent No. US20020012970A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Edward APPLICANT: Elistrom, Ca.
                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILLNG DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILE REFERENCE: RPA1006
CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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ORGANISM: Thermus sp. Z05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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1 LSQELAIPYEE 11
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TITLE OF INVENTION: Detection of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                    APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers, Thomas
Schoenbrunner, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Higuchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elistrom, Carita
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                                     Mast, Andrea L.
Brow, Mary Ann D.
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Pred. No. 0.00018;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                Sequence 2, Application US/09972834 Publication No. US20020192663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                                       1 LSQELAIPYEE 11
                     CORRESPONDENCE ADDRESS:
                                             NUMBER OF SEQUENCES:
                                                          TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FORS-02736 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                          APPLICANT: Loeb, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: CAMPBELL & FLORES LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-NOV-1996
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
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APPLICATION NUMBER: US 01
FILING DATE: 02-DEC-1996
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FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/0107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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APPLICATION NUMBER: US 08/756,386
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                                                                                                      Suzuki, Motoshi
                                                                                                                         Hood, Leroy
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                                                            of Identifying and Using Same
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; ORGANISM: Thermus aquaticus
US-10-071-505-1
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 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
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                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/148,012
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                           TITLE OF INVENTION: TAQ DNA POlymerase Have TITLE OF INVENTION: E681 and Homologs The TITLE OF INVENTION: Tolerance FILE REFERENCE: PB9944 CURRENT APPLICATION NUMBER: US/10/071,505 CURRENT FILING DATE: 2002-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Davis, Maria
                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1
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                                                                                                                   TYPE: PRT
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Local Similarity 100.0%;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                            Flick, Parke
                                                                                                                                                                                                                                                                                                                                                                            Kumar, Shiv
Finn, Patrick J.
Nampalli, Satyam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 832 amino acids
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                   Score 54; DB 9; Length 832; Pred. No. 0.02;
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Pred. No. 0.02;
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                                                                                                                                                     RESULT 10
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                                                                                            Sequence 8, Application US/10033297 Publication No. US20020187486A1
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                      GENERAL INFORMATION:
APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                         678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 LSQELAIPYEE 688
                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSQELAIPYEE
                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/682,853
FILIKG DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/081,806 FILING DATE: 22-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATION NUMBER: US/08/756,386
                                                          Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
                     Mast,
                                   Lyamichev, Victor I.
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, Andrea L.
, Mary Ann D.
                                                        Jeff G
                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                  Score 54; DB 9
Pred. No. 0.02;
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                                                                                                                                                                                                                                                                                                                   DB 9; Length 832;
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RESULT 11
US-10-033-297-66
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                                                                                                                                          Sequence 66, Application US/10033297 Publication No. US20020187486A1
                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                           1 LSQELAIPYEE 11
Brow, Mary Ann D.

TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                 APPLICANT: Hall, Jeff G.
Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FORS-02736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States Of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/599,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/682,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/823,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/350,597 FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                          Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                100.0%;
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02-DEC-1996
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Pred. No. 0.02;
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                                                                                                                                                                                             Sequence 69, Application US/10033297 Publication No. US20020187486A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
                      CORRESPONDENCE ADDRESS:
                                           NUMBER OF SEQUENCES:
                                                                                  TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/350,597
"ILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                           APPLICANT: Hall, Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQ ID NO: 66:
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
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APPLICATION NUMBER: US 01
FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/682,853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                      Lyamichev, Victor I.
Mast, Andrea L.
Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 Montgomery Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 54; DB 9; Length 833; 100.0%; Pred. No. 0.02;
                                           Sequential Invasive Cleavages : 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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US-10-033-297-71
Sequence 71, Application US/100:
Publication No. US20020187486A1
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Best Local Similarity
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSQELAIPYEE 11
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TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll,
                                                                                                                                             TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                             NUMBER OF SEQUENCES: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
         STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-No. US200: CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENCTH: 833 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/
FILING DATE: 21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/682,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/756,386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/823,516
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                                                                                                                INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolia, Diane E
                                                                                                                                                                Brow,
                                                                                                                                                                                  Mast, Andrea L.
                                                                                                                                                                                                         Lyamichev, Victor I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 54; DB 9; Length 833; 100.0%; Pred. No. 0.02; Live 0; Mismatches 0; Indels
                                                                                                                                                                Mary Ann D.
                                                                                                                                                                                                                             Jeff G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-1996
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; SEQUENCE DESCRIPTION: SEQ ID NO: 71: US-10-033-297-71
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 LSQELAIPYEE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSQELAIPYEE 11
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                   APPLICANT: Prudent, James R.
Hall, Jeff G.
Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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SEQUE 'E CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                   COUNTRY: United States Of America
                                                                                                                           STATE: California
                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 705-84
TELEFAX: (415) 397-8338
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APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
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                                                                                                                                                                        STREET:
                                                                                                                                                                                           ADDRESSEE: Medlen & Carroll, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US97/01072 FILING DATE: 21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/033,297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/756,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/758,314 FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States Of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolia, Diane E
                                                                                                                                                                   220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 54; DB 9; Length 833; 100.0%; Pred. No. 0.02;
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US-10-033-297-6
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Publication No. US20020187486A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 8:
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                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/350,597
FILING DATE: 09-Jul-1999
                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brow, Mary Ann b. Britan of Nucleic Acids By Multiple TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                  APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
APPLICATION NUMBER: PCT/US97/01072
                          APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States Of America
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                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mast, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyamichev, Vietor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 9
Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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0; Gaps

0

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FILING DATE: 21-JAN-1997

APPLICATION NUMBER: US 08/759,038

FILING DATE: 02-DEC-1996

APPLICATION NUMBER: US 08/758,314

FILING DATE: 20-DEC-1996

APPLICATION NUMBER: US 08/562,853

FILING DATE: 29-NOV-1996

APPLICATION NUMBER: US 08/682,853

FILING DATE: 12-JUL-1996

APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

ANTORNEY/AGENT INFORMATION:

NAME: IN9011a, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02736

TELEPHONE: (415) 705-8410

TELEPAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 834 emino acids

TYPE: emino acid

STRANDEDNESS: single

FOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-033-297-6

US-10-038; Score 54; D:

Mismatche:
Search completed: January 15, 2003, 12:39:50 Job time: 10.8571 secs
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                                                                                 680 LSQELAIPYEE 690
                                                                                                      1 LSQELAIPYEE 11 .. *
                                                                                                                                                              ; Score 54; DB 9; Length 834;
; Pred. No. 0.02;
0; Mismatches 0; Indels
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0;

Page 7

Sequence Sequence Sequence

12,

-07035-5

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 1, Appli

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Result
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Maximum DB
                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                              YGAPOP=10
                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein - nucleic search, using frame_plus_p2n model
                                                                                                                                      Score
                                                                                                                                                                                      d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                              -YGAPEXT=0.5 -DELOP=6 -DELEXT-7
       Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                     Match Length
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1 LSXELXIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                           /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
       DВ
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     US-08-073-384C-12

US-08-254-359A-12

US-08-483-043-12

US-08-481-238-12

US-08-471-066B-12

US-08-471-066B-12

US-08-491-7653-12

US-08-756-386-12

US-08-756-386-12

US-08-756-386-12

US-08-823-516-12

US-08-682-853A-12

US-08-759-038-12
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     RESULT 1
US-08-073-384C-12
                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08073384C Patent No. 5541311
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 04-JUN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAITOLI, Peter G.
REGISTRATION NUMBER: 32,83
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                TITLE OF INVENTION: SYNTHESIS-I
                                                                                                                                                                                                                                                                                   APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Hrow, Mary Ann D.
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                       STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                    94104
                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAVERSTOCK, MEDLEN & CARROLL
                                                                                                NUMBER: US/08/073,384C
04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS-DEFICIENT THERMOSTABLE DNA
                      £ G.
· 32,837
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                                                                    07/986,330
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US-08-254-359A-2

US-08-481-238-2

US-08-481-238-2

US-08-481-956-2

US-08-757-653-2

US-08-759-491-2

US-08-758-386-2

US-08-758-386-2

US-08-759-386-2

US-08-759-386-2

US-08-759-384-2

US-08-759-038-2

US-08-759-038-2

US-08-759-038-2

US-08-759-038-2

US-08-759-038-2

US-08-759-038-2

US-08-759-314-2

US-08-750-348-2

US-08-750-946-2

US-07-977-434-1

US-07-628-4818-1

US-07-628-4818-1
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US-09-096-399-1

US-08-648-657-1

US-08-648-657-1

US-08-648-657-2

US-09-096-399-3

PCT-US95-14418-3

PCT-US95-15327-3
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US-08-458-819-5
PCT-US91-07035-5
                     FORS-00613
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US-09-350-309-12
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Version #1.25

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US-08-254-359A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-073-384C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                  NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410]
TELEPHAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08254359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08 FILING DATE: 06-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LYAMICHEY, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5/ MUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/254,359A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                 ENGTH:
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                                                              nucleic acid
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CALIFORNIA
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                                                                               1600 base pairs
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                               linear
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                                                                                                                                                                                                                                                           NUMBER: US 07/986,330
07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
            DNA (genomic)
                                                double
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93.62%
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Best Local Similarity:
Query Match:
US-09-823-649A-2 (1-11) x US-08-483-043-12 (1-1600)
                                            Best Local Similarity:
Query Match:
                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-483-043-12
                                                                                              Score
                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-483-043-12
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                                                                             Percent Similarity:
                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08483043 Patent No. 5691142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                      TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                  : AdyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HAVERSTOCK, Machine STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuSer***GluLeu***!leProTyrGluGlu 11
                                                                                                                                                                                                                               LENGTH:
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: United States of America
                                                                                                                                                                                                                           1600 base pairs
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                                                                                          Length:
Matches:
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US-08-471-066B-12
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Query Match:
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                                                                    Sequence 12, Application US/08471066B
Batent No. 5837450
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08481238
Patent No. 5795763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                             TITLE OF INVENTION: 5' Nucleases D
TITLE OF INVENTION: DNA Polyermase
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
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APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/481,238 FILING DATE:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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Medlen & Carroll, LLP
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Percent Similarity:
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Query Match:
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REFERENCE/NOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                  Sequence 12, Application US/08484956 Patent No. 5843654
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                          APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: US 07/986,330 APPLICATION NUMBER: US 07/986,330 FILING DATH: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 04-JUN-1993
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
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ZIP: 941
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                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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Matches:
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RESULT 7
US-08-757-653-12
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Best Local Similarity:
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US-08-484-956-12
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                                                                                                                                                                                                                                                                                                                 Patent No. 5
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      APPLICANT: Kaiser, microcit.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                            TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: |
FILING DATE: 09-NOV-
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APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
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                                                                                ADDRESSEE: Medlen & Carrott, July STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JUN
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COMPUTER: II
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                                                                              California
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                                                         United States Of America
Floppy disk
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06-JUN-1994
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ingolia, Diane E.
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338
                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAME E.
REGISTRATION NUMBER: P-40,027
                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PRUDENT, JAMES R.
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GROTELUESCHEN HALL, JEFF S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                       APPLICATION NUMBER: US/08/599,491 FILING DATE: 23-JAN-1996
                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuSer***GluLeu***IleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12, Application US/08599491
5. 5846717
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                                                                                                                                                                                                                                                                                                              94104
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                                                                                                                                                                                                                                                                                                                                                                                  220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIVE, DAVID M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYAMICHEV, VICTOR
                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
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                                                                                                                                      23-JAN-1996
N: 435
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                                                          FORS-01802
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Matches:
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Pred. No.:
                 Alignment Scores:
                                                 ; MOLECULE TYPE: US-08-756-386-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                              TELEFAX: (415) 397-833 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/682,853
FILING DATE: 12-JUL-1996
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                                                                                                                                                                           TELEPHONE: (415) 397-8338
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
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                                                                                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                LENGTH: 1600 base pairs
                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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                                                                                                               nucleic acid
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EDNESS: double
                                                                                                                                                                                                                                                             Ingolia, Diane E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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Lyamichev, Victor
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                                                                                    linear
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                                                               DNA (genomic)
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Invasive Cleavge Of Nucleic Acids
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                                                                                                                                                                                                                                              40,027
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Percent Similarity:
Best Local Similarity:
Query Match:
US-08-823-516-12
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Patent No. 5>
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                                                                                                                                                                                                                            TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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                            MOLECULE TYPE:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 705-8410
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APPLICATION NUMBER: 1
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mast, Andrea J.,
APPLICANT: Brow, Mary Ann D.
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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                                                                                                                                                                LENGTH:
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                                                                                                                                                     1600 base pairs
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                     DNA (genomic)
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US-09-823-649A-2 (1-11) x US-08-682-853A-12 (1-1600)
                                                          Percent Similarity:
Best Local Similarity:
                                              Query Match:
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                                                                                                                                                                    US-08-682-853A-12
                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40,027
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8318
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US OF FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-JUL-1996
CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California...
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                                                                                                                                                                                                                    STRANDEDNESS: double
                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/682,853A
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                                                                                                                                                                                                                                                  1600 base pairs
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                                                             Mismatches:
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                                               Indels:
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US-08-758-314-12
                                                                                                            US-09-823-649A-2 (1-11) x US-08-759-038-12 (1-1600)
                   RESULT 13
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Best Local Similarity:
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US-08-759-038-12
                                                                                                                                                                      Query Match:
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                                             INFORMATION FOR SEC ID NO:
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                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1
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APPLICATION NUMBER: 1
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dahlberg, James E.
APPLICANT: Dahlberg, James E.
Cleavage Of Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/759,038 FILING DATE: 02-DEC-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                             1 LeuSer***GluLeu***IleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                            DNA (genomic)
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US-09-350-309-12
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                                                                                                                                                                                      Sequence 12, Application US/09350309 Patent No. 6348314 GENERAL INFORMATION:
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LENGTH: 1600 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 24-JAN-1996
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/01
FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LeuSer***GluLeu***IleProTyrGluGlu 11
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STATE: California
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Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids NUMBER OF SEQUENCES: 69
                                                                                                                  APPLICANT: Prudent,
Hall, Je
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nucleic acid
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220 Montgomery Street, St
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                                                                                                                                                      James R.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08520946 Patent No. 6372424
                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

APPLICANT: LYAMICHEY, VICTOR I.

APPLICANT: OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-841
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1133 CTCTCCCAGGAGCTAGCCATCCCTTACCAGGAG 1165
                                                                                        STREET: 220 BULLISCO
CITY: SAN FRANCISCO
STATE: CALIFORNIA
STATE: CALIFORNIA
STATE: STATE
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                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                      COUNTRY:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPIJCATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
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OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARK: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Medlen & Carroll, LLP
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: <Unknown>
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STATE: California
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                                                                                      UNITED STATES OF AMERICA
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAM48270
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AAW30093
                                            Bst DNA polymerase.
B. stearothermophi
Bacillus stearothe
B.stearothermophil
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Native DNA polymer
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a a a a a-	B. pallidus DNA po B. pallidus DNA po B. pallidus DNA po Enterococcus faeca E. coli cellular p Protein encoded by Lactococcus lactis Chlamydia pneumoni	mino acid sacillus callacillus	A pol us st rothe actin A pol A pol us ca rothe rothe rothe rothe rothe rothe standard

## ALIGNMENTS

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Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus caldotenax.
                                                                                    WPI; 2002-076891/11.
                                                                                                                                    Schoenbrunner NJ, Wang AM;
                                                                                                                                                            Smith ES, Elfstrom CM,
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                                                                                                                                                                                                                                                                                                        12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                            Gelfand DH,
                                                                                                                                                            Higuchi RG,
                                                                                                                                                            Myers TW;
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DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.

Native DNA polymerase motif #18 25-MAR-2002 (first entry) AAM48269;

AAM48269 standard; Peptide;

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using a mutant thermoactive DNA polymerase

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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises that, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                             Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                      Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Native DNA polymerase motif #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM48270 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA, a primer, a divalent cation, and a mutant thermoactive DNA, DNA polymerase. These motifs represent a conserved region which affects the fluorescein and cyanine family dyes. The method of the invention is provides improved reverse transcription/amplification reactions. The method concentrations relative to previous high temperature reverse transcription efficiency at lower enzyme transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides flatter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reverse transcription extension rates, and consequently less time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LAQNLNISRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences given in AAB47791-97 and AAM48259-AAM48270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                            Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               ΑM;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                              Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           žs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stearothermophilus thermostable DNA polymerase clone Bst2 which lacks the complete 5'-3' exonuclease domain. The corresp. gene was constructed by ligating the HindIII-SalI fragment from the clone pdemBst2.1sst conty is end of the gene with the Styl-HindIII fragment of the clone pdemBst2.1sst conty pdemBst5'end conty. The 5' end of the DNA polymerase gene. The styl-HindIII fragment covers the mid-region of the gene up to and exonuclease domain. The remainder of the 5' exonuclease but not the 5'-3' reconstituted by the ligated and extended oilgonucleotides AAT04816-17.

The modified DNA polymerase can be used in primer extension reactions
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1995;
01-APR-1994;
16-SEP-1994;
                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the modified Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus DNA encoding thermostable polymerase for nucleic acid sequencing and amplification  \begin{tabular}{ll} \hline \end{tabular} \begin{tabular}{ll} \hline \e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT04802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-373510/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riggs MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09527067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus; thermostable DNA polymerase; PCR; primer; amplification; probe; Bacillus caldotenax; exonuclease; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.stearothermophilus DNA polymerase variant Bst2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR80139 standard; Protein; 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR80139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase. These motifs represent a conserved region which affects DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is provides improved reverse transcription/amplification reactions. The method concentrations relative to previous high temperature reverse concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides fast reverse transcription extension rates, and consequently less time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LAQNLNITRKE 11
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DNA sequencing or polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                 Page 83-85; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sivaram M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0222612.
94US-0307410.
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.0025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                   gene was constructed pGemBst2.1sst contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 5
AAW10597
ID AAW1
                                                                                                                          Query Match
Best Local Similarity
Thes 10; Conserve
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                              stearothermophilus strain DNA polymerase. The heat stable DNA polymerase can be used in a method for the replication of a DNA chain. It can also be used in a method for the determination of the sequence of DNA chain. As the DNA polymerase has a proof reading 3'-5' exonuclease activity, possible mismatches of base pairing that occurs in current methods of DNA sequence determination of a DNA clone can be avoided.
       AAW10597 standard; Protein; 587 AA.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase from Bacillus stearothermophilus - used in DNA amplification and sequencing methods having lower frequency of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT90819
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-474304/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hong GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP09220087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW30093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW30093 standard; Protein; 587 AA.
                                                                                                                                                                                                                                                                                                                         This is the peptide sequence (587 amino acids) of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1996;
18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA replication; exonuclease; proof reading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus stearothermophilus DNA polymerase (peptides 1-587).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1998
                                                                                 432 LAQNLNITRKE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus stearothermophilus; DNA polymerase; DNA amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HONG/) HONG G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 LAQNLNITRKE 442
                                                                                                             1 LAQNLNIXRKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZHAI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang W,
                                                                                                                                                                                                     587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960S-0642584
950S-0544643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96JP-0160402
                                                                                                                                                        98.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhai F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.0%;
90.9%;
                                                                                                                                          Score 48; DB Pred. No. 0.2; 0; Mismatches
                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                       DB
                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 587;
                                                                                                                                                                      Length 587
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                        Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps
                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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       RESULT 6
AAY91931
                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus DNA polymerase (Bst Pol 1) large fragment (AAW10597) lacks the N-terminal 3'-5' exonuclease domain of native Bst Pol I. It is encoded by a DNA construct (AAT36360) obtd. by PCR cloning of genomic DNA using a primer (AAT60826) based on the large fragment N-terminal sequence (AAW10599). Recombinant Bst Pol I large fragment can be produced in transformed bost cells, esp. as a fusion protein with mallose binding protein. It is thermophilic, retaining its activity at 65 deg, and is useful for nucleic acid
/note= "modified to Thr-Pro-Leu in AAY91930" Misc-difference 421
                          Location/Qualifiers Miso-difference 341..343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding recombinant thermophilic Bacillus stearothermophilus DNA polymerase I - substantially free of 3'-5', and opt. also 5'-3' exonuclease activity
                                                                                                                                                   B. stearothermophilus 320 wild type DNA polymerase
                                                                                                                                                                                      19-JUL-2000
                                                                            Bacillus stearothermophilus
                                                                                                       Modified DNA polymerase; DNA sequencing; 3' to 5' exonuclease activity; random primer labeling; site-directed mutagenesis; wild type.
                                                                                                                                                                                                                  AAY91931;
                                                                                                                                                                                                                                            AAY91931 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aliotta JM, Kong H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP757100-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bst DNA polymerase large fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW10597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing and strand displacement amplification.
                                                                                                                                                                                                                                                                                                                        432 LAQNENTTRKE 442
                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                      1 LAQNLNIXRKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-111048/11.
                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            587 AA:
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9508-0510215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96EP-0202169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bst Pol I; thermostable enzyme; exonuclease; strand displacement amplification.
                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pelletier JJ;
                                                                                                                                                                                                                                                                                                                                                                                              . 9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34pp; English.
                                                                                                                                                                                                                                              587
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Recombinant Bst Pol I

0.2; DH 18;

Length 587; Indels

0;

Gaps

0;

밁 QΥ

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-823-649 3 (1-11) x AAT70347 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
             02-DEC-1996;
24-JAN-1996;
12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence, clone 4F, encodes a Taq DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mutTaq construct described in AAT70343. The entire mutTaq gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BstXI and BamHI, at unique sites. The 3' overhang of BstXI was trimmed to a blunt end, while the overhang of BamHI was filled in. The blunt ends were ligated together. This resulted in an in-frame deletion of 903 nucleotides. The enzyme encoded by the present protein is also referred to as Cleavase BB.
  02-DEC-1996
                                                                              22-JAN-1997;
                                                                                                         31-JUL-1997
                                                                                                                                   W09727214-A1
                                                                                                                                                                                                Nucleic acid cleavage; DNA cleavage; RNA cleavage; 5' nuclease; Taq; DNA polymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                                                                                                     AAT76647 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                           1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                            Synthetic
                                                                                                                                                                       Thermus aquaticus YT-1.
                                                                                                                                                                                                                                        Taq gene 5' nuclease clone 3F (Cleavase BB).
                                                                                                                                                                                                                                                                  14-APR-1998
                                                                                                                                                                                                                                                                                              AAT76547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-201481/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2A; Columns 79-82; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                       1 I.euSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahlberg JE,
                                                                                                                                                                                                                                                                 (first entry)
96US-0682853.
96US-0756386.
96US-0758314.
                                                     96US-0759038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0986330
93US-0073384
                                        96US-0599491
                                                                              97WO-US01072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9408-0254359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0649
54.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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AAV65786
Qγ
                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                 AAV65786;
                                                                                                                                                                    DNA polymerase; nuclease; Cleavase BB;
                                                                                                                                                                                                                                      02-РЕВ-1999
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Pred

Score:

踞:

g Qy

Ω

(THIR-) THIRD WAVE TECHNOLOGIES INC

Brow MAD, Olive DM, Dahlberg JE, Prudent JR; Hall JG, Kaiser MW, Lyamichev VI;

Thermostable structure-specific nuclease(s) - characterisation of nucleic acid sequences and acid sequences and used for detection and d variations in nucleic

Example 2; Page 245; 457pp; English

NA. It relates to methods for forming a NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' nuclease activity of various enzymes (see AAW24210-13) is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific NA sequences or specific variations of them. structure-specific nuclease preferred for use in nucleic acid cleavage methods of the invention. Mutant genes (AAT76644-47) were constructed in order to determine which portions of the Taq polymerase domain can be altered without eliminating 5' nuclease altered Thermus aquaticus DNA polymerase (Taq) gene in which nucleotides 875-1778 of the wild-type gene coding sequence are deleted. Mutant gene mutTag (see AAT76643) was used as the starting material for the construct. Cleavase BB is a thermostable activity. The invention relates to means for the detection and characterisation of nucleic acid (NA) sequences and variations This DNA sequence, denoted clone 3F or Cleavase BB, comprises an

Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;

US-09-823-649A-3 (1-11) x AAT76647 (1 1600) Query Match: DB: Best Local Similarity: Percent Similarity: Alignment Scores: Мо. : 0.0649 54.00 100.00% 100.00% 100.00% Conservative: Mismatches: Indels: Gaps: Matches: 1600 11 0 0 0

AAV65786 standard; DNA; 1600 48

(first entry)

Thermus aquaticus nuclease clone 3F (Cleavase BB) DNA.

Nucleic acid detection; multiple sequential invasive cleavage;

Thermus aquaticus strain YF-1. Synthetic.

01-OCT-1998

24-MAR-1998; 98WO-US05809

24-MAR-1997; 97US-0823516

(THIR-) THIRD WAVE TECHNOLOGIES INC

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RESULT 6
AAV53855
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                           1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brow MAD,
Mast AL,
                                                   04-JUN-1998
                                                                                                                                                  Clone 4D; Taq mutant gene; thermostable; structure-specific nuclease; mutant DNA polymerase; bacteria; fungi; protozoa; RNA virus; hepatitis C virus; HCV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNAP that has reduced synthetic activity (see AAV65783-86). Clearage of the clearage structure by the nuclease indicates the presence of specific nucleic acid sequences or specific variants. The invention further relates to methods for the separation of nucleic acid molecules based on charge, methods for the detection of non-target clearage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterisation of nucleic acid sequences, and variations in nucleic acid sequences. It also relates to methods for forming a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleotide sequence (clone 3F) codes for a thermostable nuclease (Cleavase BB) derived from the DNA polymerase (DNAP) of Thermus aquaticus (Taq). In comparison to the wild-type Taq DNAP sequence (see AAV65779), it contains an in-frame deletion of 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                   26-NOV-1997;
                                                                                  W09823774-A1
                                                                                                                    Thermus sp.
                                                                                                                                                                                                                   Nucleotide sequence of clone 4F of the Tag gene mutant.
                                                                                                                                                                                                                                                        21-DEC-1998
                                                                                                                                                                                                                                                                                        AAV53855;
                                                                                                                                                                                                                                                                                                                        AAV53855 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a single reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amplification processes, and allows many targets to be analysed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this structure in a site-specific manner, preferably using a thermostable structure-specific nuclease such as a modified Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid cleavage structure on a target sequence and cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 278; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytomegalovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                       Vavra SH;
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to means for the detection and
                   97WO-US21783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
100.00%
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 A; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1600
11
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
AAV63407
Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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Qy

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US-09-823-649A-3 (1-11) x AAV53855 (1-1600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a clone of a mutant Tag gene, used in the method of the invention. In this process thermostable structure-specific nucleases are derived from mutant DNA polymerases, which can be used for detecting mutant alleles or strains of microorganisms. The structure-specific nucleases can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mixtures, compositions and kits to treat nucleic acid, e.g. for detection of wild type and mutant alleles of genes, for detection and/or identification of strains of microorganisms such as bacteria, fungi, protozoa, especially for detection of RNA viruses such as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable structure-specific nuclease(s) derived from mutant DNA polymerase(s) — useful for detecting mutant allele(s) or strains of
   Brow MAD,
                                                                             07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                        US5837450-A
                                                                                                                                                                                                                                    Synthetic.
Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                         DNA sequence of a thermostable 5' nuclease derived from Taq polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAV63407 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 238; 472pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1996;
29-NOV-1996;
                                                                                                            06-JUN-1994;
                                                                                                                                           06-JUN-1995;
                                                                                                                                                                          17-NOV-1998
                                                                                                                                                                                                                                                                                    thermostable
                                                                                                                                                                                                                                                                                                                                                               26-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1600 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatitis C virus (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microorganisms
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                           (THIR-) THIRD WAVE TECHNOLOGIES INC
Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyamichev VI,
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                     ű
                                                                                                                                                                                                                                                                                               DNA polymerase; nucleic acid detection; Cleavase BB;
                                                                           92US-0986330.
93US-0073384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0758314.
96US-0757653.
                                                                                                            94US-0254359
                                                            95US-0471066
                                                                                                                                          95us-0471066
                                                                                                                                                                                                                                                                                  nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 A;
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54.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c;
                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 G;
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WPI; 1999-023438/02

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AAQ23998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a thermostable 5' nuclease derived from a thermostable polymerase modified to have reduced synthetic activity, where the 5' nuclease is capable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The nuclease, designated Cleavase BB, is used in a method for detecting the presence of a nucleic acid molecule. The method is used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These can be used in e.g. forensic testing or paternity determination.
                                                               28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
                                                                                                                     30-SEP-1991;
                                                                                                                                                                                                                                        old_sequence
                                                                                                                                                                                                                                                                              Thermus aquaticus.
                                                                                                                                                                                                                                                                                                         5'-3'; exonuclease;
                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase pLSG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1600
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            Abramson RD,
                                                                                                                                                                         WO9206200-A
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                                     (CETU ) CETUS
                                                                                                                                               16-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                        CORP.
            Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                               90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                     91WO-US07035
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                                                                                                                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0649
54.00
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                                                                                                                                                                                                                                                                                                         PCR; amplification; SSR; sequencing; PLCR;
                                                                                                                                                                                                                 "nucleotides
                                                                                                                                                                                                 sequence"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the polymerase enzyme produced to exhibit a different ant. of 5'-3' connuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. uncleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' connuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) casay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification conditions of a target nucleic acid sequence. Mulation of the DNA cencoding particular regions of the enzymes can be used to prepare a considered particular regions of the enzymes can be used to prepare a complete lack of activity.

See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                       28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                       old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             1168 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                  Thermus
                                                                                                                                                                                                                                                                           5'-3'; exonuclease; PCR;
                                                                                                                                                                                                                                                                                                   Mutant thermostable DNA polymerase p205A292
                                                                                                                                                                                                                                                                                                                                                            AAQ24322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of Thermus aquaticus polymerase DNA which has been mutated. The mutation, resulting in mutant pLSG8, causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in e.g. PCR,
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                                                                                30-SEP-1991;
                                                                                                            16-APR-1992
                                                                                                                                    W09206200-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuSerGlnGluLeuAlaIleProTyrGluGlu
                                                                                                                                                                                                                                                  species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                 (first entry)
                     90US-0590213.
90US-0590466.
90US-0590490.
                                                                              91WO-US07035
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                                                                                                                                                               sequence."
                                                                                                                                                                                                                                                                         amplification; SSR; sequencing; PLCR; ss
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assay son the amplification and detection of a target nucleate acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare
 28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                        1168 CTCTCCCAGGAGCTTGCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of Thermus species 205 polymerase DNA which has been mutated. The mutation designated p205A292 causes the polymerase enzyme produced to exhibit a different amt. of 5', 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA polymerases with altered 5^{\prime}-3^{\prime} exo nuclease activity - having conserved regions mutated or deleted, for use
                                     30-SEP-1991;
                                                               16-APR-1992
                                                                                       WO9206200-A
                                                                                                                                                     old_sequence
                                                                                                                                                                                          Thermus thermophilus.
                                                                                                                                                                                                                   5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
                                                                                                                                                                                                                                           Mutant thermostable DNA polymerase pTTHA292.
                                                                                                                                                                                                                                                                                                                       AAQ24?28 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
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                                                                                                                                                                                                                                                                      22-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
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 900S-0590213
900S-0590466
                                      91WO-US07035
                                                                                                                                                               Location/Qualifiers
                                                                                                               /*tag=
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Matches:
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AAZ29460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of Thormus thermophilus polymerase DNA which has been mutated. The mutation designated pTHA392 causes the polymerase enzyme produced to exhibit a different amt. of 5'.3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'.3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'.3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and forter through the second content of t
                                                                                                                                                                                                                                                                                    Thermostable DNA dependent polymerase; nuclease activity; "ag polymerase; mulant; Polymerase Chain Reaction, PCR, N-terminal domain; proteolytic; thermal stability; hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer driven mutagenesis; identification of pathogen; mutational analysis; forensic identification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
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                                                                                                                                                                                                     Thermus aquaticus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA dependent mutant Tag polymerase-1 encoding DNA
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/*tag= a
/product= "Thermostable mutant Tag
/note= "Identical at C-terminus to
                                                                                                                                      Location/Qualifiers
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from Thermus aquaticus"

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RESULT 12
AAT47959
ID AAT47
   Db
                                                                                                                                                                                                                                                                 US-09-823-649A-3 (1-11) x AAZ29460 (1-1682)
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Query Match:
                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the DNA encoding a novel, thermostable DNA dependent, mutant Taq polymerase-1 enzyme. The N-terminal domain of polymerase includes a sequence of 9 amino acids, that has 40-50% sequence identity with residues 280-288 of native Thermus aquaticus polymerase, Taq. The residues 10-53 of encoded by this sequence is identical to residues 289-832 of Taq polymerase. This sequence has ignificant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) based processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, identification of pathogens, mutational analysis and forensic
                                                                                                                                                                                                                              1202 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1234
          31-MAY-1995;
                                               04-DEC-1996
                                                                EP745676-A1
                                                                                  Thermus aquaticus
                                                                                                                                Mutant Taq polymerase FY2
                                                                                                                                                                       AAT47959;
                                                                                                                                                                                        AAT47959 standard; DNA; 1686
                                                                                                                                                                                                                                                                                                                                                            Sequence 1682 BP; 286 A; 567 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel enzyme, particularly useful in polymerase chain reaction
                            30-MAY-1996;
                                                                                                    DNA sequencing; PCR; ss.
                                                                                                                                                     11-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                 identification.
                                                                                                             polymerase; FY2; FY3; FY4; thermostable; Thermus; enzyme;
                                                                                                                                                                                                                                               LeuSerGlnGluLeuAlaIleProTyrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-105869/09
                                                                                                                                                  (first entry)
          95US-0455686
                             96EP-0303880
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RESULT 13
AAT47961
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerases providing improved results in DNA sequencing reactions. FY2 is the T. aquaticus DNA polymerase lacking pref. the 271-272 N-terminal amino acids and having the amino acid at position 667 of the wild type (Phe) replaced by Tyr. FY3 contains 562 amino acids with a Met at position 1 and Ala at position 2, corresponding to the Met and Ala of positions 271 and 272, respectively, of the wild type enzyme. FY4 corresponds to the T. thermophilus DNA polymerase lacking the N-terminal 274 amino acids having a Phe to Tyr replacement at position 396 (position 669 of the wild type enzyme).
New enzymatically active Thermus DNA polymerase(s) - having a tyrosine at a position equivalent to 667 of Taq DNA polymerase and lacking 5' to 3' exonuclease activity
                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taq; polymerase; FY2; FY3; FY4; thermostable; Thermus; enzyme; DNA sequencing; FGR; ss
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                                                                                                                                                         Davis
                                                                                                                                                                                                                                               31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Tag polymerase
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                                                                                        P-PSDB; AAW09317
                                                                                                                                                                                              (AMSH ) AMERSHAM LIFE SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1686 BP; 283 A; 567 C; 578 G; 258 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT47961 standard; DNA; 1686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing; PCR; ss
                                                                                                        1997-013699/02.
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                                                                                                                                                    Fuller CW,
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Matches:
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Indels:
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polymerase having a Tyr residue at a position corresponding to Taq DNA polymerase residue 667 in its dnmp binding site, and lacking 5' to 3' exonuclease activity as a result of an N-terminal deletion. The polymerases can be used for the sequencing of DNA, either by manual automated means.
                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1219 CTCTCCCAGGAGCTAGCCATCCCCTACGAAGAA 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY00886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1996;
31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMSH ) AMERSHAM LIFE SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FY2 polymerase coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 thermostable DNA polymerases - havin lacking 5' to 3' exonuclease activity
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                                                                                                                                                                                                                                                                                                                                                         Column 11-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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95US-0455686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
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AAX27132
ID AAX2
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Best Local Similarity:
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US-09-823-649A-3 (1-11) x AAX27132 (1-1686)
                                Query Match:
                                                                Score:
                                                                           Pred.
                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-823-649A-3 (1-11) x AAX27130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                 thermostable polymerases of the invention are variants of Taq DNA polymerase having a Tyr residue at a position corresponding to Taq DNA polymerase residue 667 in its dNMP binding site, and lacking 5′ to 3′ exonuclease activity as a result of an N-terminal delection. The polymerases can be used for the sequencing of DNA, either by manual or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1219 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1251
                                                                                                                             automated
                                                                                                                                                                                                                                 and lacking
                                                                                                                                                                                                                                                                                               Cunniff JJ,
                                                                          No.:
                                                                                                        Sequence 1686
                                                                                                                                                                                     This sequence encodes a thermostable DNA polymerase of the invention.
                                                                                                                                                                                                          Claim 4; Colomb 23 28; 27pp; English.
                                                                                                                                                                                                                                            New
                                                                                                                                                                                                                                                                 P-PSDB; AAY00888
                                                                                                                                                                                                                                                                           WPI; 1999-228538/19.
                                                                                                                                                                                                                                                                                                                                         31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                 14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX27132;
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                                                                                                                                                                                                                                                                                                                   ( HSMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                              thermostable DNA polymerases - having lacking 5' to 3' exonuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase;
                                                                                                                                                                                                                                                                                                                    AMERSHAM LIFE SCI INC
                                                                                                                           means
                                                                                                                                                                                                                                                                                               Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                                                        96US-0648657.
95US-0455686.
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                             Length:
Matches:
Conservative:
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Db Qy 

Search completed: January 15, 2003, 12:55:28 Job time: 133.143 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                       Score
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54
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1: /SIDS2/gccdatc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: *
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                                Mutant
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882333336	AA(10)575 AAR23144 AAR23162 AAR23167 AAR25565 AAR215569 AAR23143 AAR23161 AAR23166 AAR2316	AAY 4 4 352 AAR66209 AAY 4 353 AAR9544 AAR99544 AAR996205 AAW09315 AAW09317 AAY00886 AAW09316 AAY00887 AAW09310 AAR99303 AAR09305 AAR09305 AAR09554 AAR06554
Mutant thermostabl Mutant thermostabl Mutant thermostabl Mutant thermostabl Mutant thermostabl Mutant thermostabl T. aquaticus (Taq) Wild type Taq DNA Cold-sensitive mut	800 H	

## ALIGNMENTS

AAB47793 standard; peptide;

11

AAB47793;

25-MAR-2002 (first entry)

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RESULT 1
ARABH7793
ID AABH
XX AABH
XX AABH
XX AABH
XX DNA
XX IPLI
XX PHOI
PO 07-N
XX 18-P
XX 18-P
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XX HOF
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive; dye; amplification.
Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                               Smith ES, Elfstrom CM, Schoenbrunner NJ, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Native DNA polymerase motif #3.
                                                                                                                                                                                                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                   2002-076891/11
                                                                                                                                                                                                                                                    Wang AM;
                                                                                                                                                                                                                                                                                             Gelfand DH,
                                                                                                                                                                                                                                                                                             Higuchi RG,
                                                                                                                                                                                                                                                                                             Myers
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RESULT 2
AAM48259
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DAA polymerases used in the method of the invention. The method for reverse transcribing an RAA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                       Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                    Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                WPI; 2002-076891/11.
                                                                                                                                                                                                                               Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-198336P.
                                                                                                                                                                                                                                                                                                                                                        12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Native DNA polymerase motif #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48259 standard; Peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 3; 23pp; English.
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                                                                                                                                                                                                                             m СМ, Gelfand DH,
Wang AM;
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Pred. No. 0.00096;
; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
             polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleolides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides itsister.
transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster \alpha
                                                                                                                                               RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                   The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises
                                                                                                                                                                                                                                                                  Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                       using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                    WPI: 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith ES, Elistrom CM,
                                                                                                                                                                                                                                                                                                                       Reverse transcribing an kNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 20000S-198336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dye; amplification.
                                                                                                                                                                   treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; reverse transcription; primer; divalent cation; mutunt; transverse transcription reaction; iluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Native DNA polymerase motif #10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA, a primer, a divalent cation, and a mutant thermoactive DNA
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 Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Higuchi KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00096;
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RESULT 4
AAM48262
                 Best Local Similarity Matches 11; Conserv
                                                       Query Match
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                                                                                               Sequence
                                                                                                                                                                  DNA polymerase's ability to incorporate dideoxynuclectides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                                                                                         of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 7; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase; reverse transcription; primer; divalent cation; mutant) transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Native DNA polymerase motif #11.
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                                                                                                                                                    reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47791-97 and AAM48259-AAM48270 native forms of motifs derived from DNA polymerases used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-198336P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48262 standard; Peptide; 11 AA
                                                                                                                                                                                                                                                                                                       polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF') HEREMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reverse transcription extension rates, and consequently less time
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                                                                                                                                      for
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                                                                                               11 AA;
                                                                                                                                    the reaction.
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                                   100.0%;
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Pred. No.
                                 Score 54; DB 23;
Pred. No. 0.00096;
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                     Mismatches
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                   0;
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                               RESULT 6
AAR96267
                                                                                                                                                                                                                                                                 RESULT 5
AAM48264
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                                           Query Match
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             AAR96267 standard; Protein; 528 AA.
                                                                                                                                                                                                                                                                                                                 provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                Illuorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-076891/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Native DNA polymerase motif #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM48264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoenbrunner
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                                                                                                                                                                                                          Local Similarity
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                                                                                                                                  1 LSQELAIPYEE 11
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                                                                                                              LSQELAIPYEE 11
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                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                       the reaction.
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001EP-0109341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NJ, Wang AM;
                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelfand DH,
                                                                                                                                                                                      0;
                                                                                                                                                                                                        Score 54; DB 23;
Pred. No. 0.00096;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Higuchi RG,
                                                                                                                                                                                                                        Length 11;
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Matches
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                                                                                                                        Best Local Similarity
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09-NOV-1994;
09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                             Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the vector was digested with BStXI and BamHI. The DNA was after the vector was digested with BStXI and BamHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brow MAD, Dahlberg
Oldenburg MC, Olive
                                                                                                                                                                                                                              then treated with the Klenow fragment of DNAPEC1 to trim both overhangs to blunt ends which were then ligated together, result in an in frame deletion of 903 nucleotides. This mutant Tag polymerase is also referred to as the Cleavase BB enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rad1/Rad10 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2A; Page 287-288; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT27686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus; identification; detection.
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Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Thermus aquaticus DNA polymerase (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1996
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                        374 LSQELAIPYEE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
                                                               LSQELAIPYEE 11
                                                                                                                                                                                         528
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                       AA;
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95US-0402601.
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                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fors L,
                                                                                                        0;
                                                                                                                        Score 54; DB 17;
Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heisler LM,
                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyamichev VI;
                                                                                                                                              Length 528;
                                                                                                                                                                                                                                                                        resulting
                                                                                                      0;
                                                                                                      Gaps
                                                                                                      0;
                                                                                                                                                                                                                                                                      RESULT 8
AAR23163
ID AAR2
                                                                                                                                           δõ
                                                                                                      밁
                                                                                                                                                                                       Matches
                                                                                                                                                                                                             Best
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                               sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a mutant of Thermus aquaticus polymerase mutant MET-SER 290 Taq (the Stoffel fragment) having a different amt. of 5'-3' exonuclease activity than the mative enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable DNA polymerases with altered 5′-3′ exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5'-3'; exonuclease;
  AAR23163 standard; Protein; 544 AA.
                                                                                                                                                                                                                                                                                                             See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  techniques, esp. nucleic acid amplification by PCR, self-sustained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amt. of 5'-3' exonuclease activity than the native enzyme.
Thermostable DNA polymerases are useful in many recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ildM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 1..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant thermostable DNA polymerase enzyme MET-SER 290 Tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR23145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR23145 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1992
                                                                                                    390 LSQELAIPYEE 400
                                                                                                                                                                                                           Local
                                                                                                                                           1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1992-150885/18.
                                                                                                                                                                                     11;
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ23998
                                                                                                                                                                                                                                                                      544 AA;
                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       900S-0590466.
900S-0590490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0590213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "deletion of residues 2-289 of native segmence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DH;
                                                                                                                                                                                   0,
                                                                                                                                                                                                      Score 54;
Pred. No.
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                    0.076;
                                                                                                                                                                                                                        DB 13;
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g 80

RESULT 7

AAR23163

Length 544;

0; Gaps

0,

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В
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a mutant of Thermus species 205 polymerase mutant MET ALA 292 TWO5, having a different ant. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
               Thermus thermophilus
                                      5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                              Mutant thermostable DNA polymerase enzyme MET-ALA 292 Tth.
                                                                                          22-0CT-1992
                                                                                                                    AAR23168;
                                                                                                                                            AAR23168 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                 proteins having 5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus species 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant thermostable DNA polymerase enzyme MET-ALA 292 TZ05.
                                                                                                                                                                                                                                                                                                                                             See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1992 (first entry)
                                                                                                                                                                                                            390 LSQELAIPYEE 400
                                                                                                                                                                                                                                   1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1992-150885/18.
                                                                                                                                                                                                                                                                                                                   544
                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0;
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0590213.
90US-0590466.
90US-0590490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                    exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DH
                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                             Score 54; DB 13;
Pred. No. 0.076;
0; Mismatches 0
                                                                                                                                                                                                                                                                                       DB 13; Length 544;
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               0;
 ID XXX ACC PD DT XXX PD XXX
                                                                                                                                                                                                                                                               Дb
                                                                                                                                                                                                                                                                                      QY
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23-AUG-2001
                        WO200161015-A2
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RESULT 10
AAE09304
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a mutant of Thermus thermophilus polymerase mutant MET-ALA 292 Tth. having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PCCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                             Thermus aquaticus; Taq; DNA polymerase; polymerisation; PCR protocol; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombi proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key Location/Qualifiers Misc-difference 1..2
                                                                        Thermus aquaticus (Taq) DNA polymerase #1.
                                                                                                         22-NOV-2001 (first entry)
                                                                                                                                           AAE09304;
                                                                                                                                                                      AAE09304 standard; Protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-150885/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1991;
Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDH; AAQ24328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09206200-A
                                                                                                                                                                                                                                                                                                                                                                                                          See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                  390 LSQELAIPYEE 400
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                               1 LSQELAIPYRE 11
                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                       AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                           544 AA;
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelland DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9008-0590490
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90US-0590466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                           Score 54; DB 13
Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                           DB 13; Length 544;
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 11
AAY44352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA dependent polymerase; nuclease activity; "aq polymerase; mutant; Polymerase Chain Reaction; PCR; N-terminal domain; proteolytic; thermal stability; hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer driven mutagenesis; identification of pathogen; mutational analysis; forensic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated. The polymerase is thermostable and possesses new or improved catalytic properties compared to known nucleic acid polymerases. The polymerase eliminates the need to specifically develop multi-enzyme reaction mixtures, which are often difficult to optimise and expensive to use. The polymerase facilitates rapid, efficient and accurate generation of nucleic acid molecules, particularly in regard to PCR protocols. The polymerase is also useful for nucleic acid polymerisation which is useful in genetic engineering techniques and molecular biology. The protein sequence is Thermus aquaticus (Taq) DNA polymerase.
             11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 46-49; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric nucleic acid polymerase for nucleic acid polymerization and generation of nucleic acids, comprises two enzymatically active domains
                                                           16-DEC-1999
                                                                                                               W09964438-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoscable DNA dependent mutant Taq polymerase-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR- 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44352 standard; Protein; 553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-536571/59
                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a chimeric nucleic acid polymerase comprising at least two enzymatically active domains which are non-naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which are non-naturally associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loeffert D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (QIAG-) QIAGEN GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 LSQELAIPYEE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-EP01790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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             99WO-US13305
                                                                                                                                                                                                                                      Thermus aquaticus"
                                                                                                                                                                                                                     10..553
                                                                                                                                                                                                                                                                 /label= Nine_residue_domain
/note= "40-50% identical to
                                                                                                                                                             /note= "Identical to residues 289-832 of native Thermus aquaticus"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                   residues 280-288 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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  AAK66209
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XX
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AAK6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local

    1 LSQELAIPYEE 11

Claim 3; Page 39-44; 79pp; English
                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                        Barnes WM;
                                                                                                                                                                                                                                                                                                                                          19-FEB-1993;
22-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Fig 2; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ29460
                                                                                                                                                          WPI; 1995-006692/01.
N-PSDB; AAQ79545.
                                                                                                                                                                                                                                                                                      (BARN/) BARNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09426766-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR66209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR66209 standard; Protein; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-105869/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 LSQELAIPYEE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qui Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                         W M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0096399.
                                                                                                                                                                                                                                                                                                                                          93US-0021623.
94US-0021623.
                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US01867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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The present amino acid sequence is a novel, thermostable DNA dependent mutant Taq polymerase-1 enzyme. The N-terminal domain, includes a sequence of 9 amino acids, that has 40-50% sequence identity with residues 280-280 of native Thermus aquaticus polymerase, Taq. The residues 10-53 of this polymerase sequence is identical to residues 289-832 of Taq polymerase. This sequence has no significant nuclease activity, but good proteolytic and thermal stabilities and improved solubility in hydrophilic solutions. This sequence is used for synthesis of polymucleotides, particularly in polymerase chain reaction (PCR) hased processes, like sequencing, labeling, primer-driven mutagenesis, diagnosis of genetic disorders, identification of pathogens, mutational analysis and forensic identification.
DNA polymerase and formulations comprising it - allowing the amplification of sequences up to 35 kilobases and reducing the mutagenicity generated by the PCR process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable polymerase; Klentay 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel enzyme, particularly useful in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase Klentag-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 13
AAX44353
ID AAY44353
ID AAY444353
AC AA444
AC AAY44
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC Kientaq-278 is a thermostable polymerase lacking 3'-exonuclease activity. The AA sequence is substantially the same AA sequence as CC Thermus aquaticus DNA polymerase but lacks the N-terminal 280 AAS. A CC DNA encoding such a polymerase is claimed, as is the polymerase CC itself. The polymerase also has substantially the same AA sequence CC as that of Thermus flavus, but excludes the N-terminal 279 AAs. Primers AAO79543, AAO79553 and AAO79554 can be used for the CC amplification of the gene for KlenTaq-278. Essentially the same CC primers can be used for the amplification of the analagous gene from CC Thermus flavus (see AAO79543, AAO79556, AAO7957). An intiator Met and a CC Gly occupy the first two N-terminal posns of Klentaq-278, CC DNA polymerase, followed by the AA sequence of Mr. aquaticus CDNA polymerase, followed by the AA sequence of Mr. aquaticus CDNA polymerase, beginning with the AA residue at posn. 281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "nermostable DNA dependent polymerase; nuclease activity; Tag polymerase; mutant; Polymerase Chain Reaction; PCR; N-terminal domain; proteolytic; thermal stability; hydrophilic solution; sequencing; labeling; diagnosis; genetic disorder; primer-driven mutagenesis; identification of pathogen; mutational analysis; forensic identification.
                 WPI; 2000-105869/09
                                                            Wurst H,
                                                                                                                                                      11-JUN-1998;
                                                                                                                                                                                                     11-JUN-1999;
                                                                                                                                                                                                                                                                                               W09964438-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY44353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY44353 standard; Protein; 559 AA.
                                                                                                        (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                   16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable DNA dependent mutant Taq polymerase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 LSQELAIPYEE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
11; Conserv
                                                            Qui Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                    9808-0096399
                                                                                                                                                                                                     99WO-US13305
                                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermus aquaticus#
7..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /note= "Identical to residues 289-832 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Nine_residue_domain
/note= "40-50% identical with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "40-50% identical to N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Leader_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 16
Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     residues 280-288 of native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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AAR99544
            B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
polymerase enzyme retrieved from the culture supernatant. Such recombinantly produced polymerase can be used in applications such as DNA sequencing, DNA amplification, thermal cycle labelling (TCL)
                                                                    DNA encoding a thermostable polymerase can be inserted into expression vector which in turn can be used to transform cel transformed cells can then be cultured and the thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                            Swaminathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9614417-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Mueller RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 - MAY - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR99544;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present amino acid sequence is a novel, thermostable DNA dependent mutant Taq polymerase-2 enzyme The N-terminal domain, includes a sequence of 15 amino acids, that has 40-50% sequence identity with N-terminal residues of native Thermus aquaticus polymerase, Taq.
Disclosure; Page 93-95; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; thermostable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus flavus DNA polymerase I exonuclease free fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR99544 standard; Protein; 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis and forensic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel enzyme, particularly useful in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ29461
                                                                                         DNA encoding thermostable Thermus flavus DNA polymerase – useful for
                                                                                                                                        WPT; 1996-251767/25
                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR BIOLOGY RESOURCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 LSQELAIPYEE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSQELAIPYEE 11
                                            sequencing, polymerase chain reaction, thermal cycle labelling ligase chain reaction, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ligase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Fig 4; 32pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 AA;
                                                                                                                                                                                                       Nickerson DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                94US-0334640
                                                                                                                                                                                                                                                                                                                                             95W0-US14418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               universal thermal cycle labelling; UTCL;
                                                                                                                                                                                                       Piehl KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 21
Pred. No. 0.079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                       Skowron PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 15
AAR96205
ID AAR966
XX AAR966
XX AAR966
XX DAA p
XX DNA p
PA (MOLE
XX P1;
DR N-PSC
PA (MOLE
XX WP1;
DR N-PSC
PT Usefu
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                                                                                                              Query Match 100.0%; Score 54; DB 17; Length 560; Best Local Similarity 100.0%; Pred. No. 0.079; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                         The present sequence is that of a truncated Thermus flavus DNA polymerase I, which is exonuclease-free, and corresponds to amino acids 275 to 834 of AAR96203. A vector lacking the 5' one-third of the T. flavus DNA polymerase I was generated. The ATC startcodon of lacZ was brought in frame with the DNA encoding amino acids 239 to 834 of the Tfl DNA pol I holoenzyme using site-directed mutagenesis. This was used to generate the present sequence. This recombinant polymerase is thermostable and can be used in applications such as DNA sequencing, polymerase chain reaction, (universal) thermal cycle labelling and ligase chain reaction.
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase I exonuclease-free fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             universal thermal cycle labelling (UTCL) and ligase chain reaction (LCR). This fragment of the exonuclease free fragment of DNA polymerase I retains its polymerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 93-95; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biologically active fragments of Thermus Flavus DNA polymerase
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                                                                                                                                                                                                                                                                                                         chain reaction.
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406 LSQELAIPYEE 416
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                             LSQELAIPYEE 11
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Pred. No. 0.079;
Mismatches 0;
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Search completed: January 15, 2003, 11:20:14 Job time: 28.2857 secs

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seq length: 2000000000
of hits satisfying chosen parameters:
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        Issued_Patents_AA:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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PCT-US91-07035-6
US-08-08-1938-6-5
US-08-248-1938-5
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US-08-481-956-5
US-08-756-386-5
US-08-756-386-5
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US-08-458-819-6
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; Patent No. 5466591
; GENERAL INFORMATION:
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US-07-977-434-6
                                                        FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 590,213
FILING DATE: 18-SEP-1990
PRIOR APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION NUMBER: US 523,394
FILING DATE: 12-JAN-1988
FILING DATE: 12-JAN-1988
PRIOR APPLICATION NUMBER: US 143,441
FILING DATE: 17-JUN-1987
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
ADDITORATION NUMBER: US 063,509
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gelfand, Da APPLICANT: Abramson, F TITLE OF INVENTION: 5' TITLE OF INVENTION: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44440337533376
                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
                                                                                                                                                                                                          FILING DATE: 28-SEP-PRIOR APPLICATION DATA: APPLICATION NUMBER:
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 PRIOR APPLICATION DATA
                             PRIOR APPLICATION DATA:
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STREET: 34
CITY: Nutl
STATE: New
ZIP: 07110
                                       APPLICATION NUMBER: US 89 FILING DATE: 22-AUG-1986
         APPLICATION NUMBER: US 7 FILING DATE: 15-AUG-1991
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5' TO 3' EXONUCLEASE MUTATIONS
THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                            US 590,466
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                   US 746,121
                                                  US 899,241
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US-09-777-538-2
US-09-777-538-2
US-07-977-434-2
US-08-156-020-6
US-08-156-020-6
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Patent No. 5795762
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             FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
                                                                                         FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                         CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
                                                                                                                              APPLICATION NUMBER: US 590,490
                                                                                                                                                APPLICATION NUMBER: 07/977,434 FILING DATE: 23-FEB-1993
                                                                                                                                                                                                        FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
FILING DATE:
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                            APPLICATION NUMBER:
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REGISTRATION NUMBER: 31,822
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Local Similarity 90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    340 Kingsland Street
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                                                                                                                                                                                                                                                                                                                         Macintosh
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                                                 UMBER: US 590,466
28-SEP-1990
28-SEP-1990
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Pred. No. 0.
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Query Match
Best Local Similarity 70.
Thes 10: Conservative
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                                                                                                                                                                                                                                                                                      Sequence 6, Application:
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APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
TELECOMMUNICATION INFORMATION:
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                  APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                        APPLICANT: Gelfand, David H. APPLICANT: Abramson, Richard
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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APPLICATION NUMBER: US 455,611
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APPLICATION NUMBER:
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APPLICATION NUMBER: WO PCT/US90/07641
FILLING DATE: 21-DEC-1990
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APPLICATION NUMBER:
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                                                                                 Cli.
STATE: C.
94608
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 676 LSQELSIPYEE 686
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect F
                                                                                                            STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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20-SEP-1990
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RESULT 4
US-08-073-384C-5
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                                  Sequence 5, Application US/08073384C Patent No. 5541311 GENERAL INFORMATION:
                                                                                                                                                                                                                  Best Local Similarity Matches 10; Conserv
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: V
FILING DATE: 21-DEC-
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FILING DATE: 22-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PC
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AMINO ACID
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90.9%;
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Pred. No. 0.34;
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US-08-254-359A-5
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Matches 10;
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: HROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
 SOFTWARE: Palwilln Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT (NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: SYNTHESIS-D
TITLE OF INVENTION: POLYMERASE
TOTAL OF STATEMENTS: 29
                                                                                                                 COMPUTER READABLE FORM:
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                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                             MEDIUM TYPE:
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                                                                                                                                                     COUNTRY:
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                                                                                                                                                                          CALIFORNIA
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220 Montgomery Street, Suite 2200
                                                                                                                                                     UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                             Floppy disk
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90.9%;
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US/U8/254,359A
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Dahlbei
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                                                                                                            PRIOR APPLICATION UMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
                              TELEPHONE: 415/705-8410
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APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DI
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                            NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
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Local Similarity 90.9%;
nes 10; Conservation
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                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                            California
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                 415/397-8338
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                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Pred. No. 0.34;
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                                                            Matches
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Best Local Similarity
Matches 10; Conserv
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                                                                                        Query Match
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                                                                                                                                                                                                                         TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 831 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
677 LSGELSIPYEE 687
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                                                         Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                      TELEPHONE:
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                             1 LSXELSIPYEE 11
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                                                                                                                                                                             amino acid
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LYAMICHEV, VICTOR I.
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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 Mismatches

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                                                                     Score 48; DB 1;
Pred. No. 0.34;
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Pred. No. 0.34;
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                                                                                   Length 831;
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; Sequence 5, Application US/08471066B
; Patent No. 5837450

RESULT 8 US-08-471-066B-5

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Best Local Similarity
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APPLICANT:
                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                             TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
                                                                                                               APPLICANT:
                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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REFERENCE/DOCKET NUMBER: FORS-01800
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                        677 LSGELSIPYEE 687
         STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/471,066B FILING DATE: 06-JUN-1995
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Brow, Mary Ann D.
WENTION: 5' Nucleases Derived From Thermostable
                                                                                                                                            BROW, MARY ANN D.
                                                                                                           HEISLER,
                                                                                                                                                                                 DAHLBERG, JAMES E.
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                              OLDENBURG, MARY C.
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IBM PC compatible
                                          HAVERSTOCK, MEDLEN & CARROLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medlen & Carroll, LLP
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                                                                                                               LAURA
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Pred. No. 0.34;
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US-08-757-653-5
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                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08757653 Patent No. 5843669
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                     STREET: 220 .... CITY: San Francisco STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acid
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APPLICATION NUMBER: 0
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APPLICATION NUMBER: 1
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REFERENCE/DOCKET NUMBER: FORS-01801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-JUN-1994
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                                                                                                                      220 Montgomery Street, Suite 2200
                                                                     United States Of America
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PatentIn Release #1.0, Version
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                                                                                                                                         Medlen & Carroll, LLP
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90.9%;
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Pred. No. 0.34;
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                                                                                      TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                              FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
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TELEPHONE: (415) 705-8410
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NAME: Ingolia, Diane E.
                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY TITLE OF INVENTION: INVADER-DIRECTED CLEAVAGE NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                             REGISTRATION NUMBER: P-40,027
REFERENCE/DOCKET NUMBER: FORS-01802
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SOFTWARE: Patentin Release #1.0, Version #1.30
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               STRANDEDNESS:
                                TYPE: amino acid
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/599,491
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                                                   ENGTH:
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                                                 831 amino acids
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linear
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415) 397-8338
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Pred. No. 0.34;
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acid
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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677 LSGELSIPYEE 687
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                                                                                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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                            1 LSXELSIPYEE 11
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linear
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Pred. No. 0.34;
                                                                    Score 48; DB 2;
Pred. No. 0.34;
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; Sequence 5, Application US/08823516
; Patent No. 5994069

US-08-823-516-5

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RESULT 14
US-08-682-853A-5
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Best Local S
Matches 10
       Sequence 5, Application US/08682853A Patent No. 6001567
GENERAL INFORMATION:
APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-NOV-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE: 21-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Mast, Andrea L.
APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Detection Of Nucleic Acids By TITLE OF INVENTION: Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelace
                                                                                                                                                  677 LSGELSIPYEE 687
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nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/682,853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-JUL-1996
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02-DEC-1996
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US~08-759-038-5
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; Patent No. 6090543
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                            APPLICANT: Prudent, James R.
APPLICANT: Hail, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           677 LSGELSIPYEE 687
                                                                           COUNTRY:
                                                                                                STATE:
                                                                                                                 CITY:
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San Francisco

220 Montgomery Street,

Suite 2200

Medlen & Carroll, LLP

California

United States

Of America

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; MOLECULE TYPE: protein US-08-682-853A-5
                              Query Match 96.0%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Olive, David M. APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California COUNTRY: United S
                                                                                                                                         TOPOLOGY:
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1 LSXELSTPYEE 11
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220 Montgomery Street, Suite 2200
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Lyamichev, Victor
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                                                                                                                                                                                                                                                                                                                                                                                   US 08/599,491
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                                                Score 48; DB 3; Length 831; Pred. No. 0.34;
                                Mismatches
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                              Caps
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SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

RETURN APPLICATION UNIDER: US/08/759,038

FILING DATE: US-08/759,038

FILING DATE: US-08/759,038

FILING DATE: US-08/852,853

FILING DATE: 29-NOV-1996

PRIOR APPLICATION NUMBER: US 08/682,853

FILING DATE: 12-JUL-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 12-JUL-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 12-JUL-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 10-JAN-1996

PRIOR APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

ATTORNEY/AGENT INFORMATION: PORS-02574

TELEPONNE: (145) 705-8410

TELEPONNE: (415) 705
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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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        Published_Applications_AA:*
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10 US-09-823-643A-14
9 US-10-033-297-5
9 US-10-081-806-5
10 US-09-823-643A-8
10 US-09-823-643A-10
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US-09-823-649A-9
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Sequence 12, Appli
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Sequence 5, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 11, Appli
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Sequence 2, Appli
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Sequence 4, Appli
Sequence 6, Appli
Sequence 71, Appli
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-212-		-302	-017A	US-09-735-171A-2	-735-169A	17-	US-10-052-417-2	-10-053-632-	-632-	-10-052-417-	US-10-052-417-3	US-10-053-632-14	2	US-10-071-505-3	US-10-071-505-2	US-09-823-649A-2	US-09-777-430A-26	US-09-777-430A-23	US-09-777-430A-20	US-09-777-430A-15	US-09-777-430A-11	-430	1	US-10-033-297-6	US-10-081-806-8
6		Sequence 585, App	58,	2	2,	13	K)	13,	Sequence 2, Appli	4	3, 1	14	Sequence 3, Appli	w ~	2, A	2, 4	26,	23,	20,	15,		က		Sequence 6, Appli	

## ALIGNMENTS

US-09-823-649A-4

Sequence 4, Application US/09823649A Patent No. US20020012970A1 GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

Elfstrom, Carita Gelfand, David Higuchi,

Russell

Edward

APPLICANT: Smith, APPLICANT: Elfst

```
; NAME/KEY: VARIANT

; LOCATION: (3)...(3)

; OTHER INFORMATION: X is Q or G

US-09-823-649A-4
RESULT 2
US-09-823-649A-9
                                                                             β
                                                                                                            Qy
                                                                                                                                               Query Match 96.0
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Alice
TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYM
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: sequence motif
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                       1 LSXELSIPYEE 11
1 LSXELSIPYEE 11
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Schoenbrunner, Nancy
                                                                                                                                                                   96.0%; Score 48; DB 10; 100.0%; Pred. No. 0.001;
                                                                                                                                                 0; Mismatches
                                                                                                                                                 0; Indels
                                                                                                                                                                                  Length 11;
                                                                                                                                                 0;
                                                                                                                                               Gaps
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US-09-823-649A-14
Sequence 14, Application US/09823649A
Fatent No. US20020012970Al
GENERAL INFORMATION:
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US-09-823-649A-12
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                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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LENGTH: 11
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                                                                                                                                                                                   Matches
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
SOPTWARE: DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Myers, Thomas APPLICANT: Schoenbrunner, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS. FILE REFERENCE: RPAL006 CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERA: FILE REFERENCE: RPA1006
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                                                                                                                1 LSQELSIPYEE 11
                                                                                                                                   1 LSXELSIPYEE 11
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Gelfand, David
Higuchi, Russell
Myers, Thomas
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Gelfand, David
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Pred. No. 0.001;
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Pred. No. 0.00
0; Mismatches
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LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mast, Andrea L.
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; ORGANISM: Thermus filiformis US-09-823-649A-14
  Query Match 96.0%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                 FILE REFERENCE: RPA1006
CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gelfand, David
Higuchi, Russell
Myers, Thomas
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    0,
                     Score 48; DB 10
Pred. No. 0.001;
                                           DB 10; Length 11;
  0;
Caps
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0;

Sequence 5, Application US/10033297 Publication No. US20020187486A1 APPLICANT: Hall, Jeff G.
Lyamichev, Victor I.

CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages STATE: California CITY: San Francisco STREET: 220 Montgomery Street, Suite 2200 Brow, Mary Ann D. LLP

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/350,597

FILING DATE: 09-Jul-1999

APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
APPLICATION UDBER: US 08/758,314 APPLICATION NUMBER: US 08/756,386 FILLNG DATE: 29-NOV-1996 APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996

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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-033-297-5
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Best Local Similarity 90.9%;
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                                                                               INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,806
FILING DATE: 22-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94104
COMPUTER READABLE FORM:
                                      SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                    TYPE: amino acid
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/756,386 FILING DATE: <UIDKNOWD>
APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-UUL-1996
APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     St ANDEDNESS: single
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STRANDEDNESS: single
                                                                                                     TELEFAX: (415)
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                         REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                 NAME: Ingolia, Diane E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FORS-02736
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Pred. No. 0.13;
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Best Local Similarity
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DENGTH: 11
TYPE: PRT
SEQ ID NO 8
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09823649A Patent No. US20020012970A1
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Best Local Similarity 90.9%;
Matches 10; Conservative
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                            CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21 SOFTMARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ ID NOS: 21
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                                                                                                                                          TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006
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                                                                                                                                                                                                                                                                    APPLICANT: Smith, Edward APPLICANT: Elfstrom, Car
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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Wang, Alice
                                                                                                                                                                                                                                                                  Elfstrom, Carita
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Higuchi, Russell
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                                                                                                                                                                          Wang, Alice
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                                                                                                                                                                                                                                Higuchi,
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81.8%;
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Pred. No. 0.0039;
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; ORGANISM: Thermus sp. Z05
US-09-823-649A-11
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; ORGANISM: Thermus aquaticus
US-09-823-649A-8
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US-09-823-649A-11
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                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 11
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Best Local Similarity 81.4
Matches 9; Conservative
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SOFTWARE: Patentin version*3.0
SEQ ID NO 10
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                                                                                                                CURRENT APPLICATION NUMBER: US/09/823,649A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/198,336
PRIOR FILING DATE: 2000-04-18
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APPLICANT: Elfstrom, Cari
APPLICANT: Gelfand, David
                                                                                                  NUMBER OF SEQ ID NOS: 21
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                                                 LENGTH: 11
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Gelfand, David
Higuchi, Russell
Myers, Thomas
Schoenbrunner, Nancy
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Schoenbrunner, Nancy
Wang, Alice
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Pred. No. 0.0039;
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Pred. No. 0.0039;
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Publication No. US20020187486A1
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME
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                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hall
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APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                               COUNTRY: United States Of America
                                                                                                                                                                                                 STATE: California
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Lyamichev, Victor I.
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Pred. No. 0.00
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Pred. No. 0.0039;
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US-09-972-834-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09972834 Publication No. US20020192663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSXELSIPYEE 11
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,834
FILING DATE: 04-Oct-2001
CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: FORS-02736 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: NO. US20020187486A1 Relevant
TOPOLOGY: NO. US20020187486A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
3-297-4
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Loeb, Lawrence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   ZIP: 92121
                                                                                                                                                                                                                                                                                                                 CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/758,314 FILING DATE: 02-DEC-1996 APPLICATION NUMBER: US 08/756,386
FILING DATE: <Unknown>
                 APPLICATION NUMBER: 08/978,806
                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                     COUNTRY: United States
                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/759,038 FILING DATE: 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US97/01072 FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/823,516 FILING DATE: 24-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/350,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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81.8%;
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Pred. No. 0.48;
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TYPE: PRT
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; ORGANISM: Thermus equations 0s\text{-}10\text{-}071\text{-}505\text{-}1
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Publication No. US20020197211A1
GENERAL INFORMATION:
                                                                                                                                                        Sequence 4, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.8%; Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TAQ DNA Polymerase Having an Amino Acid Substitution at TITLE OF INVENTION: E681 and Homologs Thereof Exhibiting improved Sait TITLE OF INVENTION: Tolerance FILE REFERENCE: pB9944

CURRENT APPLICATION NUMBER: US/10/071,505

CURRENT FILINC DATE: 2002-02-08

PRIOR APPLICATION UNMBER: 05/148,012

PRIOR APPLICATION UNMBER: 05/148,012

PRIOR FILING DATE: 1999-08-10

NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P-UW 2873
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEPHONE: (619)535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   678 LSQELAIPYEE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 LSQELAIPYEE 688
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                  Hall, Jeff G.

Lyamichev, Victor I.

TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                    CORRESPONDENCE ADDRESS:
                                                                                                                               APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finn, Patrick J.
Nampalli, Satyam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flick, Parke
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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81.8%; Pred. No. 0.48;
tive 1; Mismatches
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/081,806
FILING DATE: 22-Feb-2002
CLASSIFICATION LONGER: US/08/756,386
FILING DATE: 22-Feb-2002
CLASSIFICATION NUMBER: US/08/756,386
FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/682,853
FILING DATE: 24-JAW-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAW-1996
APPLICATION NUMBER: US 08/599,491
REGISTRATION NUMBER: US 08/599,491
FILING DATE: 24-JAW-1996
ATTORNEY/ACENT INFORMATION:
REFERENCE/DOCKET NUMBER: PORS-02564
TELEPDROME: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acids
STRANDEDNESS:-single
                                                                                                                                                                                                                                                                                STRANDEDNESS: SINGle
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-081-806-4
Search completed: January 15, 2003, 12:39:51 Job time: 11.8571 secs
                                                                                               В
                                                                                                                                          QУ
                                                                                                                                                                                        Query Match 90.0%; Score 45; DB 9; Length 832; Best Local Similarity 81.8%; Pred. No. 0.48; Matches 9; Conservative 1; Mismatches 1; Indels
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                                                                                                                                          1 LSXELSIPYEE 11
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Page 6

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                    DB
DB
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protein search, using sw model
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length: 2000000000
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Match
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96.0
90.0
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pir3:*- *
pir4:*-
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T04556
F87631
$50809
T30452
T27289
KXRTC1
A40597
                                       C64474
S74356
A97735
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JC7337
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AE3130
AB1440
AI1082
G90229
S25321
AC1580
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Т41581
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C70133
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glutathione S-tran
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glutathione S-tran
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## ALIGNMENTS

RESULT 1 S26675

C;Species: Thermus aquaticus
C;Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 18-Jun-1999
C;Accession: \$26675; \$24929
R;Akhmetzjanov, A.A.; Vakhitov, V.A.
Nucleic Acids Res. 20, 5839, 1992

DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus

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endo-1,4-beta-gluc
                                                                                                               A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-831 <TSH>
C:Superfamily: DNA-directed DNA polymerase
C:Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                      DNA-directed DNA polymerase (EC 2.7.7.7) - Thermus aquaticus C;Species: Thermus aquaticus C;Species: Thermus aquaticus C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999 C;Accession: JX0359 R;Ishino, Y; Ueno, T; Miyagi, M.; Uemori, T.; Imamura, M.; Tsunasawa, S.; Kato, I. J. Biochem. 116, 1019-1024, 1994 A;Title: Overproduction of Thermus aquaticus DNA polymerase and its structural analys A;Accession: JX0359; MUID:95204371; PMID:7896728 A;Accession: JX0359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: DNA-directed DNA polymerase I C;Keywords: DNA binding; nucleotidyltransferase
QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-831 < A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from Th A; Reference number: S26675; MUID:93087201; PMID:1454544 A; Accession: S26675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X66105; NID:g48165; PIDN:CAA46900.1; PID:g48166
A;Note: the source is designated as Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translation not shown
                                       Query Match
Best Local S
Matches 9
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                         Local Similarity
nes 9; Conserv
1 LSXELSIPYEE 11
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10; Conserva
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                                         Conservative
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                                                          90.0%; Score 45; DB 2
81.8%; Pred. No. 0.75;
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Pred. No. 0.19;
                                       Mismatches
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                                                                                 DB 2; Length 831;
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                                       Gaps
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C;Accession: S46696
R;Latreille, P.
                                          N;Alternate names: hypothetical protein H8025.1
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                     γ
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: B86286
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                                                                                                                  hypothetical protein YHR071w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                     S46696
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J04639; NID:g155128; PIDN:AAA27507.1; PID:g155129; GB:M26480
C;Superfamily: DNA-directed DNA polymerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 18-Jun-1999
C;Accession: A33530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE005172; NID: g5103820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-832 <LAW>
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A;Title: Isolation, characterization, and expression in Escherichia coli of the DN A;Reference number: A33530; MUID:89197950; PMID:2649500
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 7; Conserv
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Matches 9; Conserv
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L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
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Pred. No. 15;
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No. 0.75;
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                 Query Match
Best Local s
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Matches
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A; Molecule type: DNA
A; Residues: 1-850 <A; FS
A; Cross-references: GB:AE000686; NID:g2983038; PIDN:AAC06656.1; PID:g2983047; GB:AE00
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
G70332
                                                                                                                                                                 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70332
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C70133
                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein aq_367 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
                                               A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein BB0267 - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: C70133
A; Gene: aq_367
                           C; Genetics:
                                                                                                                                A; Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                                         C; Accession: G70332
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A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    son, D.; Peterson, J.; Kerlavage,
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A;Cross-references: SGD:S0001113; MIPS:YHR071w
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A; Residues: 1-229 <LAT>
                                                                                                                                                                                                                                        Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                              R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC66681.1; PID:g268
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A;Description: The sequence of S. cerevisiae
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%;
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63.6%;
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Pred. No. 2.8;
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Similarity 6; Conserv

78.0%; 54.5%;

Score 39; Pred. No.

DB 2;

Length 850;

Conservative

w

Mismatches

2

Indels

0;

Gaps

0;

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genome polyprotein - Ornithogalum mosaic virus (fragment)
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                         JQ0494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 3323-2328, 2001
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                                                                                                                                                                                                                                                                                                                              A; Gene: AGR_L_436
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-474 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Reference number: A97359; PMID:11743194 A;Accession: D98157
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A;Reference number: AB2577; PMID:11743193
A;Accession: AE3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wood, D.W.; Setubal, J.C.; Kaul, erage, G.; Gillet, W.; Grant, C.;
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                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE007870; PIDN:AAK88782.1; PID:g15158531; GSPDB:GN00170:
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: melibiose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: melA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-457 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AE3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE008689; PIDN:AAL45459.1; PID:g17743164; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Yoo, H.; Tao,
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                           200 LAHDLDIPYEE 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                              Local Similarity les 7; Conserv
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nes 7; Conserv
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                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                63.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
63.6%;
                                                                                                                                                                                                                                         76.0%;
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                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                         Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
                                                                                                                                                                                                                                                                                     alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.9
2; Mismatches
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                                                                                                                                                                                                                                     DB 2; Length 474;
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; Markelz,
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ckelz, B.,
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C:Comment: This protein may be involved in the oncogenic C:Superfamily: papillomavirus E6 protein c:Keywords: DNA binding; early protein; zinc finger
                                                                     A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
                                                                                                                                                                                                A; Title: Nucleotide sequence of human papillomavirus type 31: A; Reference number: A94398; MUID:89299478; PMID:2545036
                                                                                                                                                                                                                                         C;Accession: A32444
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T. Virology 171, 306-311, 1989
                                                                                                                                                                                                                                                                                                            A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                             E6 protein - human papillomavirus type 31 C;Species: human papillomavirus type 31 A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: Saccharomyces probable membrane protein YLR106c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Murphy, L.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nypothetical coiled-coil protein - C; Species: Schizosaccharomvces com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Contains: coat protein; nuclear inclusion protein NI6; nuclear inclusion protein C;Species: Ornithogalum mosaic virus, OrMV C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
                                                                                                                                                    A; Status: translation not shown
                                                                                                                                                                              A; Accession: A32444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-4717 <MUR>
A;Cross-references: kMbL:ALO31546; PIDN:CAA20864.1; GSPDB:GN00068; SPDB:SPCC737.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 972h(-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T41581
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Best Local :
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Matches 7; Conserv
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7; Conserv
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87.5%;
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Library, September 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DH 2;
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                                                   this virus
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-11,'r',113-116,'p',118-121,'T',123-127,'H',129-281,'K',283-731,'E',733-75
A;Cross_references: MMBL:X57088; NID:g50054; PIDN:CAAA40368.1; PID:g50055
R;Korner, J.; Chun, J.; Harter, D.; Axel, R.
Proc. Natl. Acad. Sci. U.S.A. 88, 6834-6838, 1991
A;Title: Isolation and functional expression of a mammalian prohormone processing enzyme
A;Tetle: Tsolation and functional expression of a mammalian prohormone processing enzyme
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JC7337
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                                                 A; Residues: 1-609 < KOR>
                                                                                       A; Accession: A39604
                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December 1990
A; Reference number: S19165
                                                                                                                                                                                                                                                                                                                                            R; Nakayama,
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-753 < NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Cloning and functional expression of a novel endoprolease involved in A; Reference number: JX0171; MUID:92041727; PMID:1657897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proprotein convertase 1 (EC 3.4.21.93) precursor - mouse
N;Alternate names: furin homolog PC1; kexin homolog PC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Kubodera, T.; Yamashita, N.; Nishimura, A. Biosci. Biotechnol. Biochem. 64, 1416-1421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 03-Aug-2001
C;Accession: JC7337
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                         A;Cross-references: GB:M69196
                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: S19165
                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;30-66/Region: zinc finger CCCC motif F;103-139/Region zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JX0171
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: JX0171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 113/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ptrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AF217503; PID:g6694866; PIDN:AAF25444.1; PID:g6694867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LSSALEIPYDE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ELSIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotechnol. Biochem. 64, 1416-1421, 2000
Pyrithiamin resistance gene (ptrA) of Aspergillus
nce number: JC7337; MUID:20399355; PMID:10945258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-327 <KUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thiamin biosynthesis protein thil
    Gaspar,
                                                                      mkne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                               pituitary AtT-20 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%;
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    Mion,
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
    Marcinkiewicz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 149;
  M
Mbikay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prohormone cleavage enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oryzae: Cloning, characteriza
    M.; Chretien,
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A; Experimental source: cultivar Columbia; BAC clone F28J12 R; Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Band submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;167,208,382/Active site: Asp, His, F;173,401,645/Binding site: carbohyd
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A;Residues: 214-478 <581>
A;Residues: 214-478 <581>
A;Residues: 214-678 <581>
A;Note: the authors gave the codon for residue 330-Ser as CTC
R;Smeekens, S.P.; Avruch, A.S.; LaMendola, J.; Chan, S.J.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 88, 340-344, 1991
A;Title: Identification of a cDNA encoding a second putative prohormone convertase
A;Reference number: A39002; MUID:91110525; PMID:198934
                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1890 <BEV>
A; Cross-references: EMBL:AL021710
                                                                                                                                                                                                                                                                              R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, submitted to the Protein Sequence Database, February 1998
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F28J12.260 - Arabidopsis thaliana N;Alternate names: hypothetical protein F28A21.10 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #text_change 11-Jun-1999 C;Date: 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: This protein is a member of a family of subtilisin-like proteinases respon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 268, 5615-5623, 1993
A;Tittle: Purification and characterization
A;Reference number: A46622; MUID:93194858;
A;Accession: A46622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M58507; NID:9200242; PIDN:AAA39896.1; PID:9200243
A;Experimental source: pituitary AtT-20 cells
R;Seddah, N.G.; Marcinkiewicz, M.; Benjannet, S.; Gaspar, L.; Beaubien, G.; Mattei, M.
Mol. Endocrinol. 5, 111-122, 1991
                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 111-120 < ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-360,'S',362-363,'P',365-753
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A; Title: cDNA sequence of two distinct pituitary proteins homologous to Kex2 and furi A; Reference number: A35571; MUID:91000356; PMID:2169760
                          A; Reference number: 215387
                                                                                                                                                                                                                           A; Accession: T04556
                                                                                                                                                                                                                                                      A; Reference number: Z15377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T04556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Zhou, Y.; Lindberg, I.
J. Biol. Chem. 268, 5615-5623, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M58589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A37951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A37951; MUID: 91203919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pituitary compared to PC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Cloning and primary sequence of a mouse candidate prohormone convertase PC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-22, 'S', 24-753 < SMF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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7; Conserv
T04852
                                                                                                                                                                                                                                                                                                                                      T04556; T04852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 44;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the prohormone convertase PC1(PC3). PMID:8449925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMID: 2017186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 753
                                                                             Bancroft,
                                                                                                                                                                                                                                                                                                        Α.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted <MAT>
                                                                             Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                             Mewes, H.W.; May
                                                                                                                                                                                                                                                                                                           A.; Bancro
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A; Molecule type: DNA
A; Rosidues: 1-1560 <BEW>
A; Rosidues: 1-1560 <BEW>
A; Rosidues: 1-1560 <BEW>
A; Rosidues: 1-1560 <BEW>
A; Rosidues: 1-1500 <BEW>
A; Rosidues: 1-1500 <BEW>
A; Experimental source: cultivar Columbia; BAC clone F28A21
C; Genetics:
A; Map position: 4
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 150/2; 194/3; 324/3; 1470/1; 1785/1
A; Introns: 54/2; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109/1; 109
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Result
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**MODEL=frame+_p2n.model -DBW=Xlh
-Q-/cgn2_1/USPTQ_spool/US09823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB=Issued_patents_NA -QFMI=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXN=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09823649_@cGN_1_1_35_@runat_14012003_151002_29127 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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      110
121
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121
                                                                                                                                                                                                                   Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YGAPEXT=0.5
                                                                                                                                                                                                                                                                                                No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , 1
Ygapop 10.0 , 1
Fgapop 6.0 , I
Delop 6.0 , I
                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 15, 2003, 12:36:21; Search time 26 Seconds (without alignments) 129.748 Million cell updates/sec
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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US-08-471-065B-12

US-08-757-63-12

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US-08-073-384C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-DEC-1992
ATTORREY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                STREET: 220 Montgomer
CITY: San Francisco
STATE: California
COUNTRY: United State
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dahlberg, James E APPLICANT: Lyamichev, Victor APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocities
                                                                                                  APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992
                                                                                                                                                 FILING DATE: 04
CLASSIFICATION:
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Lyamichev, Victor I.
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   415/705-8410
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US-08-481-956-7
US-08-484-956-7
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US-08-757-653-7
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US-08-254-359A-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5614402
GENERAL INFORMATION:
                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: line
MOLECULE TYPE: I
             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                              TELEPHONE: (415) 705-8410]
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LYAMICHEV, VICTOR I.

APPLICANT: BROW, MARY ANN D.

TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                               LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/073,384 FILING DATE: 06-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/254,359A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: HAVERSTOCK, MEDLEN & CARROLL
1: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
                                                                                                                                                                                                                                             CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08254359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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                                   linear
             DNA (genomic)
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-823-649A-3 (1-11) x US-08-483-043-12 (1-1600)
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                                                 Best Local Similarity:
Query Match:
                                                                                                                                   Alignment Scores:
                                                                                                                                                                   ; MOLECULE TYPE: US-08-483-043-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                 Percent Similarity:
                                                                                                                  Pred. No.:
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                                                                                                                                                                                                                                                              TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 04-JUN-1993
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: United States of America
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1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11

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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                            US-08-471-066B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: US-08-481-238-12
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                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
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                                                                                                                                             Patent No. 5837450
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILLEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 harring
                                                                                                                                                                     Sequence 12, Application US/08471066B Patent No. 5837450
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APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                  TITLE OF INVENTION: 5' Nucleases De TITLE OF INVENTION: DNA Polyermase NUMBER OF SEQUENCES: 40
                                                                   APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
                                                                                                                                                                                                                                                                     1133 CYCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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MEDIUM TYPE: Floppy disk
                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
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ADDRESSEE:
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Medlen & Carroll, LLP
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Query Match:
| DB:
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                                                                                                                                                                                                                                                                                                                         US-08-484-956-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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Sequence 12, Apput.
Sequence 12, Apput.
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          1133 CHCTCCCAGGAGCTAGCCATCCTTAGGAGGAG 1165
                                                                                                                     NUMBER OF SHQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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LENGTH: 1600 base pairs
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APPLICATION NUMBER: US 08/254,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPHICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                    APPLICANT: HEISLER, LAURA TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
                                                                                                                                                                                            APPLICANT: OLDENBURG, MARY C.
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                                                                ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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CITY: San Francisco
                                                   STATE:
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                                                                                                      ADDRESSEE:
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                  94104
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                                                   CALLFORNIA
                                                                                                                                                                                                                                                                                                      Application US/08484956
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                                                                                                                                                                                                             LYAMICHEV, VICTOR I. BROW, MARY ANN D.
                                UNITED STATES OF AMERICA
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MEDIUM TYPE: Floppy disk

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US-08-757-653-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08757653 Patent No. 5843669
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INFORMATION FOR SEQ ID NO: 1
               COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 07
FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                  APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha
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                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                    ZIP: 94104
                                                                                                          STREET:
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                                                                                          ADDRESSEE: Mealen & Luiter.
STREET: 220 Montgomery Street, Suite 2200
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                                                    United States Of America
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                                                                                                                         Medlen & Carroll, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-599-491-12
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INFORMATION FOR SEQ ID NO: 12:
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                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OLIVE, DAVID M.
APPLICANT: PRODENT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GROTELUESCHEN HALL, JEFF S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BROW, MARY ANN D.
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                                                                                                                                                                                                                                                                                                         STREET: 220 MILL CITY: SAN FRANCISCO
                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                COMPUTER: 18M PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                    SOFTWARE:
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   TELEFAX:
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                                                                                    NAME:
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                                                                                                                                                  APPLICATION NUMBER:
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                                                                               INGOLIA, DIANE E.
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                                                                                                                                                                                                                                                                                                       CALLFORNIA
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                                                                                                                                                                                                                                                                                                                                      220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1600 base pairs
(415) 705-8410
(415) 397-8338
                                                                                                                                                                                                                                                                                       UNITED STATES OF AMERICA
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                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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                                                                                                                                   23-JAN-1996
                                                                                                                                                                                                                                      Floppy disk
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Indels:
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                                             ; MOLECULE TYPE: US-08-756-386-12
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               Alignment Scores:
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                                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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No.:
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TELECOMMUNICATION INFORMATION:
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                                                                              TOPOLOGY:
                                                                                          STRANDEDNESS:
                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                          FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/682,853
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/756,386
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                                                                                                                          1600 base pairs
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Lyamichev, Victor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States Of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
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SYSTEM: PC-DOS/MS-DOS
                                                                              linear
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                                                                                                                                                                                         (415) 705-8410
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                                                             DNA (genomic)
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; MOLECULE TYPE: DNA (genomic) US-08-823-516-12
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                                                                                                                                                                                                                                      TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
PILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                       (415) 397-8338
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Best Local Similarity:
US-09-823-649A-3 (1-11) x US-08-682-853A-12 (1-1600)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FOR TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/682,853A FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                          TELEFAX:
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Grotelueschen Hall, Jeff S.
Lyamichev, Victor
Olive, David M.
                                                                                                                                                                                                                                                                                         (415)
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415) 397-8338
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US-09-823-649A-3 (1-11) x US-08-759-038-12 (1-1600)
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US-08-758-314-12
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Best Local Similarity:
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APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
                                                                                                                                                                                                                       . No. :
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                         1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/759,038 FILING DATE: 02-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                1600 base pairs
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Brow, Mary Ann D.
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                                                                                                                                                                                                                                                                                                     linear
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415) 397-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              40,027
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US-09-350-309-12
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                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                Sequence 12, Applicati
Patent No. 6348314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08758314 Patent No. 6090606
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: 29-007-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Improved Cleavage Agents NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                   1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
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NUMBER OF SEQUENCES: 69
               Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
                                                                   APPLICANT: Prudent,
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San Francisco
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Lyamichev, Natasha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                  Prudent, James R.
Hall, Jeff G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1133 CTCTCCCAJGAGCTAGCCATCCCTTACGAGGAG 1165
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                        TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                   STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                COUNTRY:
                                                                                                                                                                 ADDRESSEE:
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ADDRESSEE: Medlen & Carroll, LLP
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                                                                   94104
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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TELEFAX: (415) 397-8338
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REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1600 base pairs
                                                                                                                                                                                                                                                                LYAMICHEV, VICTOR I. OLIVE, DAVID M.
                                                                                                                                                                                                                                                                                                         BROW, MARY ANN D.
                                                                                UNITED STATES OF AMERICA
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Matches:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ARTORNEY/AGENT INFORMATION:
ARE: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOXET NUMBER: FORS-01756
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-0410
TELEPHONE: (415) 705-0410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-12
                                                                                                                                                                                                   pred. No.: 0.0143
score: 54.00
percent Similarity: 100.008
best Local Similarity: 100.008
query Match: 100.008
Search completed: January 15, 2003, 12:58:42 Job time : 29 secs
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C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 18-Jun-1999
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A;Title: Overproduction of Thermus aquaticus DNA polymerase and its structural analys A;Reference number: JX0359; MUID:95204371; PMID:7896728

A;Accession: JX0359
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                                                                                                                                                                                C; Keywords: DNA binding; nucleotidyltransferase
                                                                                                                                                                                                                A;Cross-references: GB:J04639; NID:g155128; PIDN:AAA27507.1; PID:g155129; GB:M26480 C;Superfamily: DMA-directed DNA polymerase I
                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-832 <LAW>
                                                                                                                                                                                                                                                                                                                                                        R; Lawyer, F.C.; Stoffel, S.; Saiki, R.K.; Myambo, K.; Drummond, R.; Gelfand, D.H. J. Biol. Chem. 264, 6427-6437, 1989
A;Tille: Isolation, characterization, and expression in Escherichia coli of the DNA p. A;Reference number: A33530; MUID:89197950; PMID:2649500
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A; Residues: 1-831 <ISH>
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F87631 G89782 G72516

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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70332 A;Accession: G70332; Distribution of the complete general properties of the complete general properties
                                                                                                                                                                                                                                                                                       C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: G70332
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N;Alternate names: hypothetical protein H8025.1
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 29-Oct-1999
                                                                                                                                                                        Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein aq_367 - Aquifex aeolicus
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A;Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from Therm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession:
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                                                                                                                                                                                                                                                   R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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. A; Reference number: S60435; MUID: 96158062; PMID: 8585325
F911.15 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Datc: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001 C;Accession: B86286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S60435
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C;Accession: S25321; S60435; S64453; S17019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Skala, J.; Nawrocki, A.; Goffeau, Yeast 11, 1421-1427, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;68-84/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 7R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995 R; Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, F.; Nawrocki, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X61669; NID: 94588; PIDN: CAA43843.1; PID: 94589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-326 < PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: MOI.1, a Saccharomyces cerevisiae gene that is highly expressed in early stat A; Reference number: S25321; MUID:93070608; PMID:1441749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Praekelt, U.M.; Meacock, P.A.
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A; Residues: 1-850 <AQF>
                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: SGD:S0003376; MIPS:YGR144w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SGD: THI4; MOL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMH.:X72929; NID:g1823241; PIDN:CAA97157.1; PID:g1823242; MIPS:YC
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54.58;
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A; Molecule type: DNA
A; Residues: 1-452 < OKI>
                                                                                                                                                       R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori A;Reference number: A59091; MUID:99445483; PMID:10515943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gone: PABZ116
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1154
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C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: E75148
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome l of the plant Arabidopsis.
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A; Experimental source: strain Sterne
                          A;Cross-references: GB:AF065404; NID:94894216; PIDN:AAD32346.1; PID:94894258
                                                                                                  A; Status: preliminary
                                                                                                                                A; Accession: B59096
                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                          hypothetical protein pXO1-42 - Bacillus anthracis virulence plasmid pXO1 C; Species: Bacillus anthracis
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A; Residues: 1-417 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: E75148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A75001
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A;Accession: B86286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome ,stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; anonymous, Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PAB2116 - Pyrococcus abyssi (strain Orsay)
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score 37; DB 2; Length 417, Pred. No. 28;
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                                                       Query Match
Best Local :
                          Matches
                          hes 7; Conserv
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alphd-galactosidase (meliblase) [imported] - Agrobacterium tumefacions (strain C58, C;Species: Agrobacterium tumefacions (c;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 17-May-2002 C;Accession: D98157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
D98157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefacions C58
A;Reference number: AB2577; PM1D:11743193
A;Accession: AE3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Wood, D.W.; Setubal, J.C.; Kaul, erage, G.; Gillet, W.; Grant, C.; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-galactosidase melA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C; Species: Agrobacterium (umefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note\colon similar to hypothetical, glutamate rich protein; locus A45555; Plasmodium fa C;Genetics:
A; Map position: linear chromosome C; Superfamily: melibiose-specific alpha-galactosidase
                                                                                                                                                                                                                   A;Reference number: A97359; PMID:11743194
A;Accession: D98157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: linear chromosome C; Superfamily: meliblose-specific alpha-galactosidase
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                                                                                    C; Genetics:
                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-474 < KUR>
                                                                                                                                                                                                                                                                   A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                     Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                       R; Goodner, B.;
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A; Residues: 1-457 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                           A; Gene: AGR_L_436
                                                                                                           A;Cross-references: GB:AE007870; PIDN:AAK88782.1; PID:g15158531; GSPDH:GN00170
                                                                                                                                                                                            A; Status: preliminary
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nes 7; Conser
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                                                                                                                                                                                                                                                                                                                        , B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, F.; Wollom, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
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Score 37; DE Pred. No. 33;

DB 2; Length 474;

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RESULT 14
A40597
R; Gutman, P.D.; Fuchs, P.; Ouyang, L.; Minton, K.W J. Hacteriol. 175, 3581-3590, 1993
                                        C;Species: Deinococcus radiodurans
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-2000
C;Accession: A40597; E75363; S42112; S42235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid A;Reference number: 221520
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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R; Kubodera, T.
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                                                                                                                  DNA-directed DNA polymerase (EC 2.7.7.7) I - Deinococcus radiodurans (strain R1)
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A;Reference number: JC7337; MUID:20399355; PMID:10945258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:F07E5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U80837; PIDN:AAB37908.1; GSPDH:GN00020; CESP:F07E5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-412 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T34415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F07E5.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 113/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: ptrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AF217503; PID:g6694866; PIDN:AAF25444.1; PID:g6694867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JC7337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biosci. Biotechnol. Biochem. 64, 1416-1421, 2000
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Search completed: January 15, 2003, 12:37:17 Job time : 16.1429 secs

Дb

10 LRQELAIPF 18

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M.; Shen, M.; Vamalhevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI.
A; Reference number: A75250; MUID:20038896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: E75363
A;Molecule type: DNA
A;Residues: 'MYFCGDGGLSCESIDFALCCLRGRSGNYVQSRTLP',1-12,'T',14-41,'H',43-72,'F',74-92
A;Cross-references: CH:AE002012; CH:AE000513; NID:g6459473; PIDN:AAF11264.1; PID:g64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamalhevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein yxaB [imported] - Lactococcus lactis subsp. lactis (strain 11.74) (Species: Lactococcus lactis subsp. lactis C:Species: Lactococcus lactis subsp. lactis C:Date: 0.75 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C:Accession: C86902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1
C; Superfamily: DNA-directed DNA polymerase I
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A; Residues: 1-921 <GUT>
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                                                                                                                                                                            A;Gene: yxaB
                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                     A; Experimental source: strain 11,1403
                                                                                                                                                                                                                                                           A:Cross-references: GB:AE005176; PID:g12725285; PIDN:AAE06317.1; GSPDB:GN00146
                                                                                                                                                                                                                                                                                                A; Residues: 1-59 <STO
                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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A;Accession: C86902
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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    Mismatches

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                                                           Mismatches
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                                                                                                             DB 2; Length 59;
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T.; Zalewski, C.
                                                  Gaps
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Minimum DB seq length: 0
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   pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   US-09-823-649A-3
54
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length DB
POLG_OMV
POLZ_GCMV
YLIJ_ECOLI
Y564_METTH
Y110_HUMAN
MTAP_CABELL
SP84_YEAST
MYOM_APICA
MYOM_APICA
Y028_BACAN
Y028_BACAN
Y113_METUA
SYS_CABELL
S6A7_HUMAN
                                                                                                                                                                                                                        DPO1_THEFI
THI4_ASPOR
DPO1_DEIRA
VE6_HPV31
TRC5_ECOLI
KCY_AQUAE
RM08_YEAST
PANB_PSEAE
IP2B_YEAST
GLK_ANASP
MANH_CLOPE
MONDALINI
CIW5_HUMAN
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Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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Proc. Natl. Acad. Sci. U.S.A. 95:12562-12567(1998).
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EMBO J. 17:7514-7525(1998).
                    Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; DNA-binding; 3D-structure.
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.
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MEDLINE=99380545; PubMed=10449720;
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meDLINE=98445410; PubMed=9770525;
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"Crystal structures of the Klenow fragment of Thermus aquaticus DNA
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MEDLINE=98266352; PubMed=9605316;
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SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase 1, thermostable (BC 2.7.7.7) (TAC polymerase 1).
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SMART; SM00278; HhH1; 1.
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MEDLINE=93285135; PubMed=8508785;
MEDLINE=93285135; PubMed=8508785;
MEDLINE=93285135; PubMed=8508785;
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Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; DNA-binding.
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HSSP; P19821; 1TAQ.
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modified and this statement is not removed.
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ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY.
-1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
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                                                                                                                                                                                                                                                                                                   EMBL; L...

JISSP, P19921; LIAN.

InterPro; IPR002421; 5_3_exu...

InterPro; IPR001098; DNA_pol.

InterPro; IPR002298; DNA_pol!.

**The Pro; IPR000513; EXO_N.I.

**The Pro; IPR000513; HHH_I.

**The Pro; IPR000513; HHH_I.
                              Matches
                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTHETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (BC 2.7.7.7) (Tth polymerase 1).
                                                                                                                                                                                                         PRINTS; PR00868; DNAPOLI. SMART; SM00475; 53EXOC; 1. SMART; SM00278; HhH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase gene (polA) from Thermus thermophilus HB8.";
J. Ferment. Bioeng. 76:285-269(1993).
-I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                     SEQUENCE
                                                                                                                                                                              SMART; SM00279; HhH2; 1
SMART; SM00482; POLAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPOT_THETH P52028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                DNA-binding.
                                                                                                                                                 PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                              TIGRFAMs; TIGR00593; pola; 1.
                                                                                                                                                                                                                                                    Pfam; PF01367; 5_3_exonuclease; Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, nucleotide sequence, and expression in Escherichia coli of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urabe I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asakura K., Komatsubara H., Soga S., Yomo T., Oka M., Emi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermaceae; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Thermus/Deinococcus group; Deinococci; Thermales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                  Iransferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 LSQELAIPYEE 690
                            Local Similarity
nes 11; Conserv
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 1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                PF00476; DNA_pol_A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
834 AA;
                                                                                     834 AA;
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                       412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                       834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93798 MW;
                                                                                     94049 MW;
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                                                                                                                                                                                                                                                                                                                                                                       5_3_exonuclease
                                          100.0%; Score 54; DB 1; 100.0%; Pred. No. 0.011;
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                   POLYMERASE (BY SIMILARITY).
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A851FF3C3076348E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                       1A98145DC11A54A9 CRC64;
                               Mismatches
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                                                         DB 1; Length 834;
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                              0;
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                              Indels
                                                                                                                                DNA repair;
                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
                              Gaps
                            0;
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     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                            SMART; SM00475; 53EXOc; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
                                                                                                                                                                                                           TIGREAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01367; 5_3
Pfam; PF02739; 5_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; 1PR003584; HHH_2.
InterPro; 1PR001532; XPGC_Rad.
Pfam; PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celsius; can be used at temperatures up to 95 degree Celsius. -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 20:5839-5839(1992).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
Thermaceae; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
10A polymerase 1, thermostable (EC 2.7.7.7) (ffl polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPOF_THETH
                                                                                                              SEQUENCE 831 AA;
                                                                                                                                                                                      Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                           SMART; SM00485; XPGN; 1
                                                                                                                                                                                                                                                                                                        SMART; SM00482;
                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P19821; 1TAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMBL; X66105; CAA46900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- BIOTECHNOLOGY: Used in the PCR method because of its high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Thermus flavus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akhmetzjanov A.A., Vakhitov V.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93087201; PubMed-1454544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ACM B-1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-274;
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                                                                                                                                                               DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO00513; Exo_N_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPRO01098; DNA_pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and nucleotide sequence of the DNA polymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; [PR003583; HHH_].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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     hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermostability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S24929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                               409
  Conservative
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                                                                                                                                                                                                                                                                                                     POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _3_exonuclease; 1.
                                                                                                           831
93783 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Has an optimal temperature above 70 degrees
e used at temperatures up to 95 degree Celsj
                                                                                                                                                                                                                                                                                                                                                                                                                                       _exonuc_N; 1.
                          81.5%;
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    Mismatches

                          Score 44; I
Pred. No. 0
                                                                                                                                     POLYMERASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                        96F93CEFA3CA536D CRC64;
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                                                    DB 1;
                             95;
                                              Length 831
Indels
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1 LSQELAIPYEE 11

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01-FEB-1995
                                                                                                                                             THI4_YEAST STANDARD; PRT; 326 AA.
p32318;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                 Thiazole biosynthetic enzyme, mitochondrial precursor.
THI4 OR MOLI OR ESP35 OR YGR144W OR G6620.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston V., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 265:2077-2082(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vignati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCL5 OR YHR071W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG18_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 LNYELAIPYDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 LSGELSIPYEE 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIFIC CYCLINS PCLT AND PCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S0001113; PCL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S46696; S46696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U00061; AAB68375.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 AA; 26467 MW; 86839ABB9DB5DD49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclin PCL5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
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Query Match
Best Local Similarity
""" Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skala J., Nawrocki A., Goffeau A.;
"The sequence of a 27 kb segment on the right arm of chromosome VII from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, CYS4,
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- INDUCTION: REPRESSED BY THIAMINE.
-!- MISCELLANEOUS: EXPRESSED AT HIGH LEVELS IN THE EARLY STATIONARY
PHASE OF BATCH CULTURES GROWING ON MOLASSES, AN INDUSTRIAL MEDIUM.
-!- SIMILARITY: BELONGS TO THE TH14 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Praekelt U.M., Meacock P.A.;
"MOLI, a Saccharomyces cerevisiae gene that is highly expressed in early stationary phase during growth on molasses.";
Yeast 8:699-710(1992).
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                         EMBL; X61669; CAA43843.1; -.
EMBL; X85807; CAA59802.1; -.
EMBL; X72929; CAA97157.1; -.
EMBL; Z72930; CAA97159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Biol. 273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Machado C.R., Praekelt U.M., de Oliveira R.C., Barbosa A.C.,
Byrne K.L., Meacock P.A., Menck C.F.;
"Dual role for the yeast TH14 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Machado C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nawrocki A., del Bino S., Goffeau A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Dyck L., Skala J., de Wergifosse P., Purnelle B., "alla E.,
Nawrocki A., del Bino S., Goffeau A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                      CHAIN
                                                                                                                                                   Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD;
                                                                                                                                                                       Pfam; PF01946; Thi4; 1.
TIGREAMS; TIGR00292; Thi4; 1
                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics fustitute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE~98035046; PubMed-9367751,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION IN DNA DAMAGE TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIAMINE REGULATION.
MEDLINE~95028146; PubMed=7941734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEM1/CHO2, NSR1 genes and ten new open reading frames."; Yeast 11:1421-1427(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96158062; PubMed=8585325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 205-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93070608; PubMed=1441749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                          TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Praekelt U.M., Byrne K.L., Meacock P.A.;
"Regulation of TH14 (MOL1), a thiamine-biosynthetic gone of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reast 10:481-490(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOI. Biol. 273:114-121(1997).
FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIAZOLE. ALSO SEEMS TO HAVE A ROLE IN MITOCHONDRIAL DNA DAMAGE
                                                                                                                                                                                                                             S0003376; THI4
                                                                                                                                                                                                                                            $17019; $17019.
$25321; $25321.
                                                                                                                                                                                                          IPR002922; Thi4.
                                                                                  326 AA;
                  Conservative
                                                                                  34991 MW;
                             70.4%; Score 38; DB 1; 77.8%; Pred. No. 5.4;

    Mismatches

                                                                                                 FAD OR NAD (POTENTIAL)
                                                                                                                    THIAZOLE BIOSYNTHETIC ENZYME
                                                                                                                                    MITOCHONDRION (POTENTIAL)
                                                                                  843790F2CE00BF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Usage by
                                               Length 326;
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                                                                                                                                                                   Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01367; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuc_N; 1.
PRINTS; PR00868; DNAPOLT.
PRINTS; SM00475; 53EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institute. There are no restrictions on modified and this statement is not removed. Usage by and for sond or sond or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update) DNA polymerase I, thermostable (EC 2.7.7.7) (TFI polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DRC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98170158; PubMed=9509419;
Jung S.E., Choi J.J., Kim H.K., K
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBI, AF030320; AAC46079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus filiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-276;
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678 LSQELGIDYKE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 QELEIPYED 135
                                                                                                                                                                                                      Local
                                                                                 1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cells 7:769-776(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SM00278; EhH1; 1.
; SM00279; HhH2; 1.
; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19821; 1TAQ.
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                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TICR00593; pola; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                              833 AA;
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                          833 F
; 93890 MW;
                                                                                                                                                                                                 70.4%;
72.7%;
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                                                                                                                                                                   ٠.
                                                                                                                                                                                                 Pred
                                                                                                                                                                                                                                                                                                                          POLYMERASE (BY SIMILARITY). 51BF8B0417EEFC4D CRC64;
                                                                                                                                                                                                      Score 38; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                            DB 1; Length 833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Gutman P.D., Fuchs P., Ouyang L., Minton K.W.; "Identification, sequencing, and targeted mutagenesis of a DNA polymerase gene required for the extreme radioresistance of
                                                                                                                                                                                                                                                                                                                                 1752027:

01-007-1996 (Rel. 34, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/aunounce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterization and application as a dominant selectable marker tor transformation.";
                                                                                  MEDI.INE=93273728; PubMed=8501062;
                                                                                                              STRAIN=R1
                                                                                                                                                                                                                                                                           Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                  DNA polymerase I (EC 2.7.7.7) (POL I). POLA OR DR1707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPO1_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF217503; AAF25444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THIA OR PTRA.
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                                                                                                                                        SEQUENCE OF 36-956 FROM N.A
                                                                                                                                                                                              NCBI_TaxID=1299;
                                                                                                                                                                                                                        Deinococcaceae; Deinococcus
                                                                                                                                                                                                                                              Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Milochondrial (Potential).
-1- SIMILARITY: BELONGS TO THE THI4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosci. Biotechnol. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kubodera T., Yamashita N., Nishimura A.;
"Pyrithiamine resistance gene (ptrA) of Aspergillus oryzae: cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-HI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Bungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THI4_ASPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 ELGVPYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ELAHYEE II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIAZOLE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01946; Thi4; 1.
AMS; TIGRO0292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35099 MW;
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIAZOLE BIOSYNTHETIC ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64:1416-1421(2000)
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                                                                                                                                                                                                                                              group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 956 AA.
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Pfam; PP00476; DNA_POLA; 1.
Pfam; PP01367; 53_exonuclease;
Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long % \left( 1\right) =\left( 1\right) +\left( 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00475; 53EXOc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; DR1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L14581; AAC36974_1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
803 LSNDLGIPYAE 813
                                                                                                                                                                                  Local
                                                                     1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the FMBL outstation \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P19821; 2KTQ.
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                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000513;
IPR003583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR00593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002421; 5_3_exonuclease.
IPR001098; DNA_pol.
                                                                                                                                                                                                                                                                                                                                                                                       Exonuclease; DNA-binding; Complete proteome.

48
T - A (IN REF. 1).

77
77
77
H -> D (IN REF. 1).

108
108
F -> L (IN REF. 1).

118
128
P -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                  406
540
956
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HhH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF11264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNAPOLI
                                                                                                                                                                                                                                                                                                                                                                108
128
406
                                                                                                                                                                                                                                                                                              105659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long as its content
                                                                                                                                                                                  66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pola;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_polI.
                                                                                                                                                                              Score 36; DB 1;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                             -> R (IN
-> R (IN
-> V (IN
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                              6ABBF117D75AB84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                    REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                 Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIS DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s.
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                                                                                                                                                   Gaps
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RESULT 10 VE6\_HPV31

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Best Local
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P17386;
01-AUG-1990
01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of human papillomávirus type 31: a cervical neoplasia-associated virus.";

Virology 171:306-311(1989).
-i- EUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
-i- EUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE OF THE UNIT OF THE ORDER OF
                Miele L., Strack B., Kruft V., Lanka E.; "Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751.";
                                                                                                                                                                                                                                                                             Escherichia coli. Plasmid IncP-beta R751
                                                                                                                                                                                                                                                                                                                                   TRAC
                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA primase trac (EC 2.7.7.-) (Replication primase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRC5_ECOLI STANDARD P27190; P27191; P27185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=89299478; PubMed=2545036; Goldsborough M.D., Disilvestre D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E
DNA Seq. 2:145-162(1991).
                                                                                                MEDLINE=92297959; PubMed=1818755;
                                                                                                                                  STRAIN=HB101
                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 2-11; 219-234 AND 702-714
                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; Pr00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J04353; AAA46950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein.
                                                                                                                                                                                                     NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early protein; DNA-binding; Nuclear protein; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! SUBCELLULAR LOCATION: Nuclear matrix-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 LSSALETPYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDED DNA (IN VITRO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A32444; W6WL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 15, Last sequence update) (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 P
139 P
; 17713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismalches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 
Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1448 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple G.F., Lorincz A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÀΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        AQUAE
                                                                                                                                                                                                                                                                                                                                                                       KCY_AQUAE
067907;
                                                                                     Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aguifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFERRED INTO THE RECIPIENT CELL DURING BACTERIAL CONJUGATION.
CATALYZES THE SYMPHESIS OF SHORT OLIGORIBONUCLECTIDE PRIMERS WITH
CPA OR PCPA AT THEIR 5'-TERMINI ON A SINGLE STRANDED TEMPLATE DNA.
-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TRAC-2 (SHOWN HERE), TRAC-3 AND
TRAC-4; ARE PRODUCED BY ALTERNATIVE INITIATION.
                                                                                                                                                                                                                                                             CMK OR AQ_2153.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: REQUIRED FOR AUTONOMOUS REPLICATION IN ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.

    SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
    SIMILARITY: BELONGS TO THE CYTIDYLATE KINASE FAMILY. SUBFAMILY 1.

                                                         Nature 392:353-358(1998).
                                                                                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                            Cytidylate kinase
                                                                                                                                                                                                                                                                                                                             16-0C:r-2001
                                                                                                                                                                                                                                                                                                                                      15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59794; CAA42460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas C.M.;
                                                                                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA replication; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO PLASMID INCP-ALPHA RP4 TRAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 QYLAVPYEQ 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QELAIPYEE 11
                                            CATALYTIC ACTIVITY: ATP + (d)CMP = ADP + (d)CDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S37669; S37669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01751; Toprim;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U67194; AAC64468.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00493; TOPRIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1448 AA;
                                                                                                                                                                                                                                                                                                                           (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                           37, Created)
37, Last sequence update)
40, Last annotation updat
(EC 2.7.4.14) (CK) (Cytid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%;
                                                                                                                                                                                                                                               Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158950 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA PRIMASE, ISOFORM TRAC-2.
DNA PRIMASE, ISOFORM TRAC-3.
DNA PRIMASE, ISOFORM TRAC-4.
FOR ISOFORM TRAC-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DE
Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1C0EAE67CD0D4ED4 CRC64;
                                                                                                                                                                                                                                                                                                           n update)
(Cytidine monophosphate kinase)
                                                                                                                                                                                                                                                                                                                                                                                        222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1448;
                                                                                                                      Aujay M., Huber
                                                                                                                                     Lenox A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p22353,
p1-AUG-1991 (Rel. 19, Created)
Ol-FEB-1995 (Rel. 31, Last sequence update)
Ol-CCT-1996 (Rel. 34, Last annotation update)
Mitochondrial 60S ribosomal protein LB (YmL8).
                                            EMBL; X53841; CAA37834.1; -. EMBL; Z34288; CAA84060.1; -. EMBL; Z49338; CAA89354.1; -.
                                                                                                                                                                                                                                                                                                                       Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.; "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Kinase; ATP-binding; Complete proteome.
NP_BIND 7 15 ATP (HY SIMILARITY).
SEQUENCE 222 AA; 25400 MW; 523BDCDFB48128C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstath the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of nuclear genes for two mitochondrial ribosomal proteins in Saccharomyces cerevisiae."; Nucleic Acids Res. 18:1521-1529(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000775; AAC07867.1;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95282514; PubMed=7762302;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90221879; PubMed-2183197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0017; cmk;
                                                                                                                                                                                                                                                                                           Yeast 11:57-60(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KM08_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003136; Cytidylate_k
Pfam; PF02224; Cytidylate_kin; 1.
                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 ISQKLNIPYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P23863;
                                                                                                                                                                                                     the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grohmann L., Graack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytidylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DI
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. -R., Isono K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA
                                                                                                                                                                There are no restrictions on 
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage by and for commercial
                                                                                                                                               Usage
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S0003599; MRPL8 \$14890; \$14890. \$47128; \$47128.

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PARSECULY 14
PANNB_PE
ID PANNB_CE
ID PANNB_CE
ID PANNB_CE
ID 16-CCT
DT 16-CCT
DT 16-CCT
DT 3-meth
DE (Ketop
GN Pseudo
OC Pseudo
OC PSeudo
OC STRALW
RX MEDLIN
RX MEDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. Tuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:959-964(2000).

-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropantoate.
-!- PATHWAY: Pantothenate blosynthesis; first branch; first step.
-!- SIMILARITY: BELONGS TO THE PANB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen 1.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M T., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANB_PSEAE
Q913C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01196; Ribosomal_L17;
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02548; Pantoate_transf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004587; AAG04987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garber R ..., Coltry L., Tolentino E., Westbrock-Wadman S., Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01167; RIBOSOMAL_L17; 1.
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                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                            Pantothenate biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Ketopantoate hydroxymethyltransferase)
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   197 LSEELAIP 204
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                                                       1 LSQELAIP 8
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                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                  TIGR00222; panB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR00059; L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                IPR003700; Pantoate_transf.
                                                                                                                                                                                                                           273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
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                                                                                                                  Conservative
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45.5%;
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26945 MW; Al30EFD95E8719BA CRC64;
                                                                                                                                                                                                                                 29802 MW;
                                                                                                                                                 63.0%;
                                                                                                                                              500
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                                                                                                                                                                    Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
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                                                                                                                                                                                                                                    B04678CE4EA5E11C CRC64;
                                                                                                                  Mismatches
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                                                                                                                                                                          DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage by and for commercial
                                                                                                                  0;
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                                                                                                                  0;
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InterPro; IPR002735; eIF5\_eIF2B.
Pfam; PF01873; eIF5\_eIF2B; 1.
ProDom; PD004078; eIF5\_eIF2B; 1.

S0006158;

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RESULT 15
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EMBL; M21813; AAA34589.1; -. EMBL; Z67751; CAA91607.1; -. EMBL; Z73594; CAA97959.1; -. PIR; S29368; S29368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Withe European Bioinformatics Institute. There are no resti
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-!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
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Donahue T.F., Ciqan A.M., Pabich E.K., Valavicius B.C.;
"Mutations at a Zn(II) finger motif in the yeast eIF-2 beta gene
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01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
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Eukaryola; Fungi; Ascomycola; Saccharomycolina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE EIF-2-BETA / EIF-5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97313271; PubMed-9169875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEX HINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL SUBUNITY TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY HYDROLYSIS OF THE GTP BUNND TO EIF-2 AND RELEASE OF AN EIF-2-GDP BINARY COMPLEX, IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER ROUND OF INITIATION, THE GDP BOUND TO FIF-2 MGST EXCHANGE MITH GTP BY MAY OF A REACTION CATALYZED BY EIF-2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
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KW Initiation factor; Protein biosynthesis; Zinc-finger.
FT DOMAIN 16 23 LYS-RICH (BASIC).
FT DOMAIN 49 56 LYS-RICH (BASIC).
FT DOMAIN 82 89 LYS-RICH (BASIC).
FT ZN.FING 236 262 C4-TYPE (POTENTIAL).
SQ SEQUENCE 285 AA; 31574 MW; 34DE9323876CEE95 CRC64;
Query Match
Best Local Similarity 45.5%; Pred. No. 28;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1.5QELAIPYEE 11
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Db 123 IQQEVGLPYSE 133

Search completed: January 15, 2003, 11:21:21
Job time: 8.28572 secs
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Q99X18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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                  Q8svp8 en Q9cdk0 Q9jeu9 Q9ckq5 n Q9a3w3 Q99x18 Q99x18 Q98c69
                                                                                                                                                                                          Q9ref0
P91228
                                                                                                                                                                                                                                                        Q9xi48 arabidopsis
Q9v1tl pyrococcus
Q9x312 bacillus an
                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                          Q8u6z1 agrobacteri
Q9ref0 bradyrhizob
P91228 caenorhabdi
                                                                                                                                                                                                                                                                                                                    Q8xs63 ralstonia s
O66691 aquifex aeo
                                                                                                                                                                     encephalito
                                       staphylococ
thermoanaer
                    rhizobium l
                                                                                  caulobacter
                                                                                                     pasteurella
                                                                                                                            human immun
                                                                                                                                                 Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
Q8XS63
Query Match
Best Local Similarity
"hatches 7; Conserve
                                                                                                     ADD DE CONTROL OF THE CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"IREARTO, PROSONIA, CON/POT_Metransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8XS63 PRELIMINARY; PRT; 519 AA.
Q8XS63;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable bifunctional: precorrin-3 methyltransferase and precorrin-6x reductase oxidoreductase protein (EC 2.1.1.131).
CBIJH OR RSP0618 OR RS03749.
                                                                                                                                            Pfam; PF02571; CbiJ; 1.
Pfam; PF00590; TP_methylase; 1.
TIGRFAMs; TIGR00715; precor6x_red; 1.
                                                                                                   Transferase; Methyltransferase; Plasmid; Complete proteome SEQUENCE 519 AA; 55892 MW; ED701EC2F7D56392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634
747
757
757
805
986
989
1230
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1531
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422
461
475
                                72.2%;
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) Q93YS5
Q9NJ08
P77542
Q937B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 Q9KEL7
7 Q8TXR1
Q93NQ2
Q93WR8
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Q92FP6
Q8YAQ3
Q8TMG8
Q94849
Q9484964
Q94973
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Q8RSH6
Q9JP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YA31
Q59971
Q989F3
           Score 39; DB Pred. No. 27; 2; Mismatches
             ν,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Database

Sequence:

Q9a4i8 caulobacter Q92fp6 listeria in Q8yaq3 listeria mo Q8tmg8 methanosarc

Q937b6 pseudomonas Q9xie2 arabidopsis Q8rsh6 uncultured

Q9jp28 pseudomonas

Q8txr1 methanopyru Q93mq2 escherichia Q93wr8 medicago va

Q94964 drosophila Q94973 drosophila Q94849 drosophila

Q9kel7 bacillus ha

Q9cxb2 mus musculu Q59311 clostridium

Q9v1y0 pyrococcus

Q9v115 drosophila Q9u3z6 drosophila

Q93ys5 arabidopsis Q9nj08 drosophila P77542 escherichia

Q941b4 oryza sativ Q44755 borrelia bu P97150 escherichia

Q9ya31 aeropyrum p Q59971 streptomyce Q989f3 rhizobium 1

on:

Result

DB 16; Length 519;

0; Gaps

0,

1 LSQELAIPY 9

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RESULT 2
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ACCOMENTATION
ACCOMENTATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9X148;
Q1.NOV-1999 (TrEMBLrel. 12, Created)
Q1.NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1.JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00052; DUF2; 1.
TIGRPAMS; TIGR00254; GGDEF; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00565; ERAL; L.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
EMBL; AE000686; AAC06656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XI48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. SEQUENCE 850 AA; 97669 MW; C02DCEF91DBCDEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001633; EAL.
InterPro; IPR000160; GGDEF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein AQ_367.
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Federspiel N.A., Theologis A.;
                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 LAQELALPY 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SREMDVPYEE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                         Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; 54.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              850 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.,
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RT DR SW SQ
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QSVII
QSVII
ID USVI
AC QSVI
DT 01-M
D
QΥ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                     01-NOY-1999 (TrEMBLrel. 12, Created)
01-NOY-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding.
SPOHENCE 1451 AA; 163602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC_tran; 2
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STRAIN=STERNE;
                                                                                                                                         Bacillus anthracis.
Plasmid virulence plasmid PX01
                                                                                                                                                                                                        PXO1-42.
                                                                                                                                                                                                                                                                            Q9x312;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                   Q9x312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00471; HDc; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 417 AA; 47906 MW; 59C62CB32C441833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9V1T1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VIT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000006; ABC_transportr; 1.
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InterPro; IPR003439; ABC_transportr.
                     SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=1392;
                                                                                                  Bacillaceae;
                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01966; HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003807; ME_Pplase_HDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ248284; CAB49268.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein PAB2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 LSNELSVPYDK 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LSQELNLHYEE 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euryarchaeota; Thermococci; Thermococcales; Thermococcaccae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLICE1. 13, Created)
(TrEMBLICE1. 13, Last sequence update)
(TrEMBLICE1. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Jobservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                          Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.58;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.48;
54.58;
                                                                                                                   Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DE
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                452 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Chapman P., Clendenning J., Deatherage G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of pXOI, the large Bacillus anthracis plasmid harboring the anthrax toxin genes.";
J. Bacteriol. 181:6509-6515(1999).
                                                                                                                                                                    "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001). "EMBL; AE009355; AAL45459.1; ALT_INIT. EMBL; AE009320; AAK88782.1; -.
                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp N., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens (strain C58 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-galactosidase.
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                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                         Cielo
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:2317-2323(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=176299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome of the natural genetic engineer Agrobacterium tumefaciens
200 LAHDLDIPYEE 210
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                                  1 LSQELAIPYEE 11
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                                                                                                                                                                                                                                                         C., Slater S.
                                                                                 Similarity
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                                                                                                                                     474 AA;
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                                                                  Conservative
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63.6%;
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63.6%;
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                                                                                   Pred. No.
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                                                                                                     DB 16; Length 474;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9REF0;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical 46.7 kDa protein.
F07E5.9.
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01-MAY-1997 (TrEMBLITEL 03, Last sequence update)
01-DEC-2001 (TrEMBLITEL 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                           None;
                                                                                                MEDLINE=99069613; PubMed=9851916;
                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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EMBL; Y09633; CAH60666.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phosphatidylcholine levels in Bradyrhizobium japonicum membranes are critical for an efficient symbiosis with the soybean host plant.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20082837; PubMed=10613857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-110SPC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-375;
Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 LSKDLATHAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 182:14-22(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s in Bradyrhizobium japonicum.";
Gen. Genet. 254:195-206(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JPR000868; Isochorismatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ('onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narberhaus F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babst M., Hennecke H., Fischer H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152ED79DACA1A2E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 9
Q8SVP8
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                                        RESULT 10
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                                                                                                                                                                                         Matches
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU04_1610.
  Q9CDK0
                                                                                                                                                                                                                                                                                                                                                           Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., Bl Alaqui H., Peyret P., Saurin W., Gouy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; U80837; AAB37908.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology. The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                Nature 414:450-453(2001).
EMBL; AL590444; CAD25350.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-GB-M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encephalitozoon cuniculi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8SVP8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002086; Aldehyde_dehydr_GLU; UNKNOWN_1
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                        Initiation factor; Hypothetical protein SEQUENCE 627 AA; 72118 MW; BBC37862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du Z., Goela D.;
                                                                                                         472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 7; Conserv
                                                                                                                                                                                                         Local Similarity
                                                                                                                                               1 LSQELAIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSQELAIPYEE 11
                                                                                                       LSEELSVAYED 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISPELAVPNEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  PRELIMINARY;
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63.6%;
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                                                                                                                                                                                                           54.5%;
                                                                                                                                                                                                                                  66.7%;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                  Score 36; DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36;
                                                                                                                                                                                                           Pred. No. 1.3e+02;
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    PRT;
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  59 AA.
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                                                                                                                                                                                                                                  Length 627;
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                                                                                                                                                                                                                                                                        RESULT 11
Q9JEU9
ID Q9JEU9
ID Q9JEU
D7 01-02
D7 01-02
D7 01-02
D7 01-02
D8 IHUMAN
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RN [1]
RN [1]
RN SEQUE
RZ STRAL
RX MEDLI
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                                                                                                                                                                                       Best Local Similarity Matches 6; Conserv
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  Q9CKQ5
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Arch. Virol. 144:2291-2311(1999).
EMBL; AF120196; AAF68138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          Congo."
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaquchi-Kabata Y., Taniquchi Y., Ido E., Kaptue L., M'pelle P., Parra H.J., Ikeda M., Hayami M., Miura T.; "Genetic diversity of HIV-1 group M from Cameroon and Republic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JEU9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9JEU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolotin A., Wincker P., Mauger S., Jailio
Weissenbach J., Ehrlich S.D., Sorokin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YXAB OR LL2219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20129484; PubMed-10664385;
Mboudjeka I., Bikandou B., Zekeng L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CNG30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21235186; PubMed=11337471; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-IL1403;
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                                                                                                         47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LRQELAIPF 18
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                                                                                                                                               1 LSQELAIPY 9
                                                                                                       IAQELGIPY 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                             IPR001584; Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AA; 7043 MW;
                                                                                                                                                                                                                                                                          95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                          10490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.8%;
77.8%;
                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                                64.8%;
                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80903DC52808162A CRC64;
                                                                                                                                                                                                                             Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No.
                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                          AFB8FD5EC6765D32 CRC64;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takehisa J., Harada Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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Length 95;

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Length 59 Indels

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                             Matches
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                               Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
                                                                                                                                                                                                                                             Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Potocka I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Wolf A., Vanathevan J., Ermolaeva M., White O., Calberg M. Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutathione S-transferase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Comple 3 genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE0005192; AAK03635.1; -.
                                                                                     SEQUENCE
                                                                                                     Transferase;
                                                                                                                                                                                                      Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9A3W3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9A3W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02798; GST_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLTNE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PM70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                        MEDLINE=21173698;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-155892;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-747;
                                                                                                                                                 InterPro;
                                                                                                                                                             InterPro; IPR004046; GST_Cterm.
                            Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LLKELAIPFE 29
1 LSQELAIPYE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSQELAIPYE 10
                                                                                                                                                                             CC3088;
                                                                                                                                                                                          AE005972; AAK25050.1;
                                                                                                                                            IPR004045; GST_Nterm.
                                                                                       208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
l protein PM1551.
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                    Complete proteome.
08 AA; 22885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Complete proteome.
12 AA; 23180 MW; 5E6D95AE3FE02E73 CRC64;
                                                                                                                                                                                                                                                                                                                                           PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                         / CB15;
                                          64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                              alpha subdivision; Caulobacter group;
                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                          Score 35; DB
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                     A48AC2988C284DD1 CRC64;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AA
                                                        DB 16; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 202;
                            ښ<u>ـ</u>
                             0;
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                             Gaps
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909X18
900X18
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      Q8RB89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanabisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TREMBLrel. 21, Created)
01-JUN-2002 (TREMBLRel. 21, Last sequence update)
01-JUN-2002 (TREMBLRel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99X18
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong Tan H., Chen R., Wang J., Yu J., Yang H.;
                                                                                                                SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                                                                                                                                                                                                            Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.aureus (strain Mu50), an MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SAV0203.
SAV0203 OR SA0197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99X18;
                                                                                       MEDLINE=21992816; PubMed=11997336;
                                                                                                                                                                                                              NCBI_TaxID=119072;
                                                                                                                                                                                                                                          Thermoanaerobacteriales; Thermoanaerobacteriaceae;
                                                                                                                                                                                                                                                                                                                                 IYASE.
ILVE OR TTE0933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8RB89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
Hypothetical profein; Complete profeome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 357:1225-1240(2001).

EMBL; AP003358; BAB56365.1; -.

EMBL; AP003129; BAB41418.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_Tax ID=158878,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; 1PR003439; ABC_transportr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 SQKEVIPYBE 239
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18 LLEELSLPYE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 240;
                            X., M
                                                                                                                                                                                                                                                                      Clostridia;
                     Ma Y., Ling
                                                                                                                                                                                                                                          Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N315);
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RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:889-700(2002).
DR EMBL; AE013059; AAM24189.1; -
KW Transferase; Aminotransferase; Complete proteome.
SQ SEQUENCE 291 AA; 32346 MW; 105072D27AB06FFE CRC64;
Query Match
Best Local Similarity 54.8%; Score 35; DB 16; Length 291;
Best Local Similarity 54.5%; Pred. No. 92;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 4; Mismatches 1; SQELAIPYEE 11
Db 218 IARELNIPFEE 228
Search completed: January 15, 2003, 12:35:45
Job time: 32.5714 secs
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Run on:

SUMMARIES

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OM protein - nucleic search, using frame_plus_p2n model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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-MODEL=frame+_p2n.model -DEV=x1h
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the Lotal score distribution.
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54
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                               W09429482-A
                                                                                                                     Thermus aquaticus YT-1.
                                                                                                                                                        DNA-polymerase; DNAP; Taq; DNA cleavage; RNA cleavage; 5' nuclease; ds.
                                                                                                                                                                                                  5' Nuclease from Tag DNAP.
                                                                                                                                                                                                                                          19-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                  AAQ80745;
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22-DEC-1994

ALIGNMENTS

7054322	SCOTE 5010 5014 5014 5014	atch 000.0 00.0 00.0 00.0 00.0 00.0	835 600 600 600 600 600 600 600 600 600	DB 16 17 17 18 18 19 19	ID
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella; Staphylococcus; identification; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Tag DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/selection protocol was used to isolate clone 4B containing a mutated Tag DNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
30-AUG-1995;
09-NOV-1994;
                                                                                                                           09-NOV-1995;
                                                                                                                                                                                                      23-MAY-1996
                                                                                                                                                                                                                                                                                         W09615267-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant Thermus aquaticus DNA polymerase coding sequence (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 95-96; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brow MAD, Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT27686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT27686 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of the resulting 5' nuclease is given in AAQ80745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l LeuSerGlnGluLeuAlaIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0073384.
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94US-0337164
                                       95US-0520946
                                                                                                                           95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                    /product= Mutant DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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Qy

US-09-823-649A-3 (1:11) x AAT27686 (1-1600)

1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165

leuserGheGluleuAlalleProTyrGluGlu 11

Query Match:

Best Local Similarity: Percent Similarity:

100.00% 100.00% 100.00%

Caps: indels: Mismatches: Conservative:

AAT70347 RESULT 3 ď

AAT70347 standard; DNA; 1600 BP

Thermus aquaticus

Synthetic

03-APR-1998 (first entry)

AAT70347;

Synthesis deficient Taq DNA polymerase gene clone 4F.

Cleavase BB; DNA cleavage; reduced synthetic activity; ss. DNA polymerase; taq polymerase gene; DNAP; 5' nuclease activity;

```
Alignment Scores:
                                                                                                                                                                                                                                   genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPEC1 to trim both 3' overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. The resulting mutant
                                                                                                                                                                                                                                                                                                                        The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternatively, microbial genc sequences. Cleavage products ar compared to the cleavage products of reference gene sequences, method is used for detecting mutation in the rman p33 gene; f
                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oldenburg MC, Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                       Sequence 1600 вР; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase, Escheri
Radl/Radl0 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2A; Page 257-258; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR96267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                   Taq polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying strains of microorganisms, especially bacteria selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli ExoIII and the Saccharomyces cerevisiae complex. The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0402601.
95US-0484956.
                                                                                                         0.0649
                                                                                    54.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fors L, Heisler LM, Lyamichev VI;
                                                                                    Matches:
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US-09-823-649A-4 (1-11) x AAQ24008 (1-2043)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermostable DNA polymerases with altered 5'-3' exo nuclactivity - having conserved regions mutated or deleted, in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated pSPSd2-151 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
Mutant thermostable DNA polymerase pspsd2-73.
                                                        22-OCT-1992 (first entry)
                                                                                                                    AAQ24007;
                                                                                                                                                                             AAQ24007 standard; DNA; 2277
                                                                                                                                                                                                                                                                                                 1576 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-150885/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2043 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
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                                                                                                                                                                                                                                                                                                                                                    1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590213.
90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 A; 697 C; 703 C; 304 T; 0 other;
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                                                                                                                 AAQ24006
                                                                                                                                                    RESULT 5
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                                                                                                                                                                                                         1810 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated pSPSd2-73 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
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                               AAQ24006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2277 BP; 378 A; 779 C; 779 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60
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28-SEP-1990;
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                                                                                        AAQ24006 standard; DNA; 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1992
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sequence."
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RESULT 4

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                        Thermus species sps17
                                                 5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
                                                                         Mutant thermostable DNA polymerase pSPSd2-199.
                                                                                                                                                                                                     1168 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           has been mutated. The mutation designated pSPSdA288 causes the polymerase enzyme produced to exhibit a different amt. of 5 - 3 exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp.
                                                                                                                                                   AAQ24009 standard; DNA; 1899 BP
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1635 BP; 267 A; 572 C; 559 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 59; 185pp; English.
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                                                                                                   22-OCT-1992 (first entry)
                                                                                                                            AAQ24009;
                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ23993-Q24013, AAQ24320-36 and AAQ24343-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity - having conserved regions mutated or deleted, for use
in e.g. PCR, sequencing and detection assays
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28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of Thermus species sps17 polymerase DNA which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in enzymes used in homogeneous assays for the amplification and
                                                                                                                                                                                                                             1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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90US-0590466
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        5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR; ss
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US-09-823-649A-4 (1-11) x AAQ24009 (1-1899)
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                1432 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of Thermus species sps17 polymerase DNA which has been mutated. The mutation designated psp82d-199 causes the polymerase enzyme produced to exhibit a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA
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Mutant thermostable DNA polymerase pSPSd2~151.
                                                                                                                                                                     AAQ24008 standard; DNA; 2043 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1899 BP; 320 A; 647 C; 647 G; 285 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerases are useful in many recombinant DNA techniques, esp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-150885/18
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                                                           22-OCT-1992 (first entry)
                                                                                                                   AAQ24008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to a complete lack of activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostable DNA polymerases with altered 5'-3' exo nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR23156.
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                                                                                                                                                                                                                                                                                                                                        1 LeuSer***GluLeuSerIleProTyrGluGlu 11
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90US-0590466.
90US-0590490.
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AAQ92369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermostable polymerase modified to have reduced synthetic activity, where the 5' nuclease is tapable of cleaving a linear nucleic acid duplex structure to create a single, single-stranded cleavage product. The methods are used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to
Key
                                                                        Thermus filiformis.
                                                                                                                                        DNA-polymerase; Tfil; thermostable enzyme; ss
                                                                                                                                                                                                                    Tfil DNA-polymerase.
                                                                                                                                                                                                                                                                                                28-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2496 BP; 402 A; 830 C; 854 G; 410 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes a method for detecting the presence of a nucleic acid molecule. The method uses a thermostable 5' nuclease derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a thermostable DNA polymerase enzyme. The sequence is used in the course of the invention. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brow MAD,
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06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1994;
07-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                AAQ92369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ92369 standard; DNA; 2512 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used in e.g. forensic testing or paternity determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dahlberg JE,
                                                                                                                                                                                                                                                                                                    (first entry)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.27
48.00
90.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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AC XX DT AC XX XX AC XX

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AAQ86927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotidyltransferase DNA-directed enzyme) which has reverse-
transcriptase activity in the presence of Mg2+. The enzyme is a
versatile DNA-polymerase suitable for use in DNA synthesis from DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                         2034 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2512 HP; 415 A; 862 C; 854 G; 381 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reactions are performed in the same buffer. The salt tolerance and is also suitable for use in
22-AUG-1986;
                                 11-APR-1995
                                                                                                                                                                                 Thermus species sps17.
                                                                                                                                                                                                                                                                                       05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                     AAQ86927 standard; DNA; 4947 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and RNA templates, and for automated DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence encodes thermostable DNA-polymerase Tfil (DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Fig 1; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995
                                                                  US5405774-A
                                                                                                                                                                                                                 Polymerase; Thermus; enzyme; thermostable; exonuclease;
                                                                                                                                                                                                                                                   Tsps17 polymerase gene.
                                                                                                                                                                                                                                                                                                                       AAQ86927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequencing using dye-primers and dye-terminators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptase activity in the presence of magnesium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New heat-stable DNA polymerase from Thermus filiformis - has reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergquist PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PACI-) PACIFIC ENZYMES 1993 LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09514770-A
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                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         93NZ-0250288
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86US-0899241.
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/*tag=
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                                                                                             /product= Thermostable polymerase
                                                                                                                  /*tag=
                                                                                                                               1246..3738
                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The enzyme has a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cycled fluorescent
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1993;
22-AUG-1986;
17-JUN-1987;
12-JAN-1988;
15-MAY-1990;
28-SEP-1990;
5' Nuclease(s) derived from thermostable DNA polymerase(s) - cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the thermostable polymerase of Thermus species sps17. It may be mutated to encode an Asp residue at position 43 instead of the wild type Gly residue. This substitution is shown to result in a 100 fold decrease in the 5'-3' exonuclease activity with no change to the polymerase activity of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                      3316 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA for Thermus species sps17 DNA polymerase - modified to encode an N-terminal deletion to reduce 5'\cdot 3' exo:nuclease activity
                                                                                                                                             06-JUN-1994;
                                                                                                                                                                                                                                                                 5' Nuclease from Taq DNAP
                                                                                                                                                                                                                                                                                                                                        AAQ80745 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4947 BP; 822 A; 1601 C; 1774 G; 750 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                WPI; 1995-036504/05.
                                                                                                                      04-JUN-1993;
                                                                                                                                                                                           W09429482-A
                                                                                                                                                                                                                                         DNA-polymerase; DNAP; Taq;
                                                                                                                                                                                                                                                                                          19-JUL-1995
                                                                                              (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                 Thermus aquaticus YT-1.
                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuSer***GluLeuSerIleProTyrGluGlu l1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columns 5-12; 26pp; English.
                                                                      Dahlberg JE,
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gelfand DH, Greenfield IL;
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86US-0899241.
87US-0063509.
88US-0143441.
                                                                                                                      93US-0073384.
                                                                                                                                             94WO-US06253.
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90US-0590213
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48.00
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                                                                      Lyamichev VI;
                                                                                                                                                                                                                                            DNA cleavage; RNA cleavage; 5' nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                       3348
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4947
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PRESENTATION OF A CAMPACA AND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-823-649A-4 (1-11) x AAQ80745 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Taq DNA-polymerase (DNAP) gene was amplified by PCR. Amplified fragments were ligated into pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter. An amplification/selection protocol was used to isolate clone 4B containing a mutated Taq DNAP gene (mutTaq) (sequence given in AAQ80746) having mormal 5' nuclease activity but less than 18 of the wt Taq DNAP activity. mutTaq was cut from pTTQ18 by EcoRI-SalI digestion and cloned into pET-3c. Thus Clone was digested with Bs(XI and Bam:I. The DNA was treated with DNAPBCI Klenow fragment and GNTPS, blut-ended and religated, resulting in an in-frame deletion of 903 nucleotides. The DNA
                                                                                                                                                                                                                                                                                                                                               30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 95-96; 159pp; English.
                                                                                WPI; 1996-259862/26.
P-PSDB; AAR96267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1600 BP; 287 A; 518 C; 553 G; 242 T; 0 other;
                                                                                                                                                                    Oldenburg MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia; Saccharomyces; Campylobacter; Staphylococcus; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Thermus aquaticus DNA polymerase coding sequence (Clone 4F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT27686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT27686 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of the resulting 5' nuclease is given in AAQ80745
                                                                                                                                                                                                                                                           (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09615267-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
                                                                                                                                                                                                   Dahlberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                       Olive
                                                                                                                                                                                                                                                                                                                94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                                                             95US-0520946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
14..1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- Mutant DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*1 ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.97
45.00
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                                                                                                                                                                       JE,
                                                                                                                                                                                                                                                              INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                Heisler LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative: Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium; Shigella; ds.
                                                                                                                                                                                                Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1600
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Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and

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AAT70347
ID AAT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-823-649A- (1-11) x AAT27686 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia, Mycobacterium, Salmoenla, Shigella and Staphylococcus. Escherichia, Mycobacterium, Salmoenla, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus and simian immunodeficiency virus. Thermus aquaticus (Taq) DNA polymerase was amplified using two primers (AAT27679, AAT27680). The Taq polymerase DNA was inserted into the BamHI restriction site of the expression vector pET-3c and mutant genes were created from that construct. This mutant was created after the vector was digested with BstXI and BamHI. The DNA was then treated with the Klenow fragment of DNAPEcl to trim both 3' overhangs to blunt ends which were then ligated together, resulting in an in frame deletion of 903 nucleotides. The resulting mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RYM) But enzyme, Thermus aquaticus DNA polymerase, "Hormus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
                                                                                                                                               07-DEC-1992;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Radi/RadiO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or
   Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase; taq polymerase gene; DNAP; 5' nuclease activity; Cleavase BB; DNA cleavage; reduced synthetic activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staph
                                                                     (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                            06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                       US5614402-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthesis deficient Taq DNA polymerase gene clone 4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT70347 standard; DNA; 1600 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taq polymerase is also referred to as the Cleavase BB enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2A; Page 257-258; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LeuSer***GluLeuSerIleProTyrGluGlu 11
   Dahlberg JE,
                                                                                                                                           92US-0986330.
93US-0073384.
                                                                                                                                                                                                                                                            94US-0254359
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Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
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Example 2; Page 245; 457pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-823-649A-4 (1-11) x AAT70347 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT76647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                     Brow MAD,
Olive DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1133 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAG 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sites. The 3' overhang of BstXi was trimmed to a blunt end, while the 5' overhang of BsmH! was filled in. The blunt ends were ligated together. This resulted in an in-frame deletion of 903 nucleotides. The enzyme encoded by the present protein is also referred to as Cleavase BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence, clone 4F encodes a Tag DNA polymerase enzyme that has normal 5' nuclease activity, but reduced synthetic ability. This sequence was derived from the mulTag construct described in AAT70343. The entire mutTag gene was cut from the plasmid, and cloned into pET-3c. This clone was digested with BstXI and BamHI, at unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable 5' nuclease derived from thermostable polymerase - has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-201481/18.
                                                                                                                                                                                                                                                02-DEC-1996;
24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      Thermus aquaticus YT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid cleavage; DNA cleavage; RNA cleavage; 5' nuclease; Taq; DNA polymerase; Cleavase BB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tag gene 5' nuclease clone 3F (Cleavase BH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT76647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT76647 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1600 HP; 286 A; 519 C; 553 C; 242 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2A; Columns 79-82; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduced synthetic activity useful in nucleic acid detection assays
                             acid sequences
                                           characterisation of nucleic acid sequences and variations in nucleic
                                                        Thermostable structure-specific nuclease(s) - used for detection and
                                                                                       WP1; 1997-393613/36.
                                                                                                                                                                   (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                 02-DEC-1996;
                                                                                                                                                                                                                12-JUL-1996;
29-NOV-1996;
                                                                                                                                                                                                                                                                                            22-JAN-1997;
                                                                                                                                                                                                                                                                                                                            31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                          W09727214-AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                       Prudent JR;
                                                                                                                                    Dahlberg JE,
                                                                                                                                                                                                96US-0758314.
                                                                                                                                                                                                               96US-0756386.
                                                                                                                                                                                                                                                                                              97WO-US01072.
                                                                                                                                                                                                                             95US-0682853.
                                                                                                                                                                                                                                                9608-0599491.
                                                                                                                                                                                                                                                               96US-0759038.
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45.00
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                                                                                                                                      Hall JG, Kaiser MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indels:
                                                                                                                                      Lyamichev VI;
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cc cleavase BB, comprises an cc altered Thermus aquaticus DNA polymerase (Taq) gene in which cure concleotides 875-1778 of the wild-type gene coding sequence are cd deleted. Mutant gene mutTaq (see AAT76643) was used as the starting cm material for the construct. Cleavase BB is a thermostable ct structure-specific nuclease preferred for use in nucleic acid cleavage methods of the invention. Mutant genes (AAT7644-47) cc were constructed in order to determine which portions of the Taq cc were constructed in order to determine which portions of the Taq cc were constructed in order to determine which portions of the Taq cc characterisation of nucleic acid (NA) sequences and variations in cc characterisation of nucleic acid (NA) sequences and variations in the target sequence and cleaving the NA cleavage structure on cc site-specific manner. The 5' nuclease activity of various enzymes cc structure, thereby indicating the presence of specific NA sequences or specific variations of them.
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Sequence 1600 BP; 286 A; 519 C; 553 G; 242 T; 0 other;

Qy 1 LeuSer***GluLeuSerTleProTyrGluGlu 11             :::	US-09-823-649A-4 (1-11) x AAT76647 (1-1600)	Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity: Query Match: DB:
LeuSer***GluLeuSerIleProTyrGluGlu                ::: M                 CTCTCCCAGGAGCTAGCCATCCCTTACGAGGAC	x AAT76647 (1-	5.97 45.00 90.91% 81.82% 90.00%
luGlu 11       AGGAG 1165	1600)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
		1600 9 1 1 0 0

search completed: January 15, 2003, 12:55:32
Job time : 134.143 secs

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-WODEL-frame+_DZN_model_DEV=xlh
-Q=/cgn2_1/USPTO_spoo1/US09823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-Q=/cgn2_1/USPTO_spoo1/US09823649/runat_14012003_151002_29127/app_query.fasta_1.1393
-DB=Issued_Patents_NA -QFWI=fastap -SUFFIX=rii -MINMATCH=0.1 -LOOPC1=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -NANTRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWI=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09823649_@CGN_11_1_35_@runat_14012003_151002_29127 -NCPU=6 -ICPU=3
-USERS-US09823649_@CGN_11_35_@runat_14012003_151002_29127 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MANP -LARGEQUERY -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXI=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                        Result
No.
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Maximum DB seq
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
   nucleic search, using frame_plus_p2n model
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length: 2000000000
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
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Match Length
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                  /ogn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-458-819-5
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US-08-073-384C-2
US-08-073-384C-2
US-08-481-238-2
US-08-481-238-2
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App.		1, App	equence I, App	equence 1, App	equence 3, App	equence 3, App	equence 3, App	equence 2, Appl	equence 14, App	equence 1, Appl	e 1, Appl	12, App	12, App	12, App	12, App	12, App	12, App	e 12, App	12, App	12, App	12, App	12, App	e 12, App	e 12, App	e 12, App	12, App	2, Appl	equence 2, Appl	equence 2, Appl	Sequence 2, Appli	ce 2, Appl	equence 2, Appl

## ALIGNMENTS

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; Sequence 5, Application US/07977434 ; Patent No. 5466591
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gelfand, I APPLICANT: Abramson,
                                   FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5:
FILING DATE: 28-SEP-1990
                                                                                                            APPLICATION NUMBER: US 590,490 FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 590,466
                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 2.1 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE:
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SOFTWARE: WordPei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 Kingsland Street
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                                                                                                                                                                                                                                                                                                                                       Macintosh
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                                                            us 590,
    US 523,394
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                                                                                         Sequence 5, Application US/08458819 Patent No. 5795762
                                                                      GENERAL INFORMATION:
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TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 5:
APPLICANT: Gelfand,
APPLICANT: Abramson,
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 2493 base pairs
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APPLICATION NUMBER: U
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REGISTRATION NUMBER: 31,822
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                                                       Gelfand, David H
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 THERMOSTABLE DNA POLYMERASES
                 , Richard D.
5' TO 3' EXONUCLEASE MUTATIONS OF
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Matches:
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Indels:
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INFORMATION FOR SEQ ID NO:
           MOLECULE
HYPOTHETICAL: NO
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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ORIGINAL SOURCE:
                                             MOLECULE TYPE:
                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                                                          LENGTH:
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                                                             TOPOLOGY:
                                                                            STRANDEDNESS: single
                                                                                                TYPE:
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07110-1199
                                                                                           nucleic acid
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                                                                                                                                                          (510) 814-2972
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gelfand, David H. APPLICANT: Abramson, Richard TITLE OF INVENTION: 5' TO 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2026 CTCTCCCAGGAGCTCTCCATCCCCTACGAGGAG 2058
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
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MEDIUM TYPE: Floppy disk
                  PRIOR APPLICATION DATA:
                                                                  PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
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APPLICATION NUMBER: 1
FILING DATE: 28-SEP-
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APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
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APPLICATION NUMBER:
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                              APPLICATION NUMBER: FILING DATE: 21-DEC
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APPLICATION NUMBER:
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California
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5' TO 3' EXONUCLEASE MUTATIONS
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                                                WO PCT/US90/07641
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 US 585,471
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US-08 073-384C-2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                 APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor APPLICANT: Brow, Mary Ann D.
                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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ANTI-SENSE: 1
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                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                 APPLICATION NUMBER: FILING DATE: 04-JUI
                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         MEDIUM TYPE:
                                                                                                                                                                          CITY: San Francisco
STATE: California
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CLASSIFICATION:
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                                                                                                                                                                                                       220 Montgomery Street, Suite 2200
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                                                                                                                                                         United States of America
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                                                                                                         Floppy disk
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 07/986,330

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                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
APPLICATION NUMBER: US 07/986,330
APPLICATION PRIOR 1992
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ATTORNEY/AGENT INFORMATION:
           REFERENCE/DOCKET NUMBER: FORS-01000 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410]
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DE
TITLE OF INVENTION: DNA POLYMERASE
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                                                                                                      FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/073,384
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OPERATING SYSTEM: PC-DOS/MS-DOS
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 TELEFAX:
                                                                   NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
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T: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
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BROW, MARY ANN D.

VENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
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(415) 397-8338
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                                                                                                                                                               TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 2:
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
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APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
                                                                                         2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Palance
                                                                                                          1 LeuSer***GluLeuSerIleProTyrGluGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FO
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; Sequence 2, Applica ; Patent No. 5843654
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                                                                                                                                                               US-08-484-956-2
                                                                                                                                                                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                           GENERAL INFORMATION:
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
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                   APPLICANT: DAHLBERG, JE
APPLICANT: LYAMICHEV, V
APPLICANT: DAMM, MARY A
APPLICANT: OLDENBURG, M
APPLICANT: HEUSHER, LAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
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APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
                                                                                                                                                                                                                    2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Release #1.0
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: California
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                                                                                                                                            Application US/08484956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2496 base pairs
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               HEISLER,
                                                      BROW, MARY ANN D.
                                                                  DAHLBERG, JAMES E.
LYAMICHEV, VICTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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                                   MARY C.
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                                                                      VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/073,384
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RESULT 10
US-08-757-653-2
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                                                                                                                     Sequence 2, Application US/08757653
Patent No. 5843669
                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                2029 CTCTCCGGGGAGCTTTCCATCCCCTACGAGGAG 2061
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LENGTH: 2496 base pair
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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APPLICATION NUMBER: 1
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APPLICATION NUMBER: US 0
FILING DATE: 09-MAR-1995
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NUMBER OF SEQUENCES:
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nucleic acid
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                                                                                     Kaiser, Michael W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-599-491-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2029 CICTCCGGGGGAGCTTTCCATCCCCTACGAGGAG 2061
               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                APPLICANT: PRUDENT, JAMES R.
THITLE OF INVENTION: DETECTION OF NUCLEIC ACID
THILL OF INVENTION: INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
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                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GROTFLUESCHEN HALL, JEFF S. APPLICANT: LYAMICHEV, VICTOR
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/757,653
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                                                                                                                                                                        STATE:
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APPLICATION NUMBER: US/08/599,491
                                                                                             MEDIUM TYPE:
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CALIFORNIA
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                                                                                                                                                     UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                             OLIVE, DAVID M.
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FILING DATE: 2 CLASSIFICATION:

23-JAN-1996

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Query Match: DB:
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INFORMATION FOR SEQ ID NO:
                 TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 2:
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                                                                                                     PRIOR APPLICATION NUMBER: US 08/599,491
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                     REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 2496 base pairs
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APPLICATION NUMBER: US 08
FILING DATE: 12-JUL-1996
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SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: P-40,027
REFERENCE/DOCKET NUMBER: FORS
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415) 397-8338
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Best Local Similarity:
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REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                  FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 29-NOV-1
PRIOR APPLICATION DATA:
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TOPOLOGY: lin
                                                      REGISTRATION NUMBER:
                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 12-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Brow, Mary Ann D.
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                                                  40,027
                                    FORS-02736
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US-09-823-645A-4 (1-11) x US-08-823-516-2 (1-2496)
US-08-682-853A-2
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             STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: D
                                                                                                      TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                 FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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APPLICANT:
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TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY ITTLE OF INVENTION: INVADER-DIRECTED CLEAVAGE
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/U: FILING DATE: 12-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                               NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-759-038-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 08/682.853
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REGISTRATION NUMBER: 40
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COMPUTER: 1HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NVENTION: Cleavage Of Nucleic Acids
SEGUENCES: 134
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Lyamichev, Victor I.
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Search completed: January 15, 2003, 12:58:46 Job time : 30 secs

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Y928_METJA
PUR6_BACSU
T1011_HUWAN
IDI1_MESAU
IDI1_RAT
ACKA_HELPJ
TNR3_MOUSE
NECI_HUMAN
CADC_HUMAN
CADC_HUMAN
VB66_BPA18
TBFC_HELN1
YLIJ_ECOL1
YPD5_CAEEL
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P80194 thermus cal
P52028 thermus the
P38794 saccharomyc
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## ALIGNMENTS

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PIR; S2493; S2493.  PIR; S2493; S24675.  HSSP; P19821; 1TAQ. InterPro; IPR002121; 5_3_exonuclease. InterPro; IPR001098; DNA_pol. InterPro; IPR001098; DNA_pol. InterPro; IPR001313; EXO_N.I. InterPro; IPR0013584; HHH_1. InterPro; IPR0013584; HHH_2. InterPro; IPR0013584; HHH_2. InterPro; IPR001352; XPGC_Rad. Pfam; PF00476; DNA_pol_A; 1. Pfam; PF00476; DNA_pol_A; 1. Pfam; PF01367; 5_3_exonuc_lease; 1. Pfam; PF02739; 5_3_exonuc_lease; 1. SMART; SM00475; 53EXOC; 1. SMART; SM00475; 53EXOC; 1. SMART; SM00475; 53EXOC; 1. SMART; SM00475; HHH1; 1. SMART; SM00479; HHH2; 1.	(I)NA)(N) COTECHNOI Dermostab SCELLANE SCELLANE SCELLANE SISSES MILLARITY MILS-PRC 20 20 20 20 20 20 20 20 20 20 20 20 20	POLA OR POL.  Thermus therrophilus.  Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;  Thermaceae; Thermus.  NCBI_TaxID=274;  [1]  SEQUENCE FROM N.A.  STRA.IN=ACM B-1257;  MEDLINE=30807201; PubMed=1454544;  Akhmetzjanov A.A., Vakhitov V.A.;  "Molecular cloning and nucleotide sequence of the DNA polymerase gene from Thermus flavus.";  Nucleic Acids Res. 20:5839-5839(1992).  -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate	TH F_THE APR-1 APR-1 JUN-1 JUN-1

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TIGREAMS;
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Eom S.H., Wang J., Steitz T.A.;
"Structure of Taq polymerase with
                                                                                                                                                                                                                                                                                                                                                                Korolev S., Nayal M., Barnes W.M., di Cera E., Waksman G.; "Crystal structure of the large fragment of Thermus aquaticus polymerase I at 2.5-A resolution: structural basis for thermostability.";
"Crystal structures of open and closed forms of binary and ternary complexes of the large fragment of Thermus aquaticus DNA polymerase
                                                        MEDLINE=99077817; PubMed=9857206;
Li Y., Korolev S., Waksman G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation, characterization, and expression in Escherichia coli the DNA polymerase gene from Thermus aquaticus.";
J. Biol. Chem. 264:6427-6437(1989).
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PROSITE; PS00447; DNA_POLYMERASE_A; 1.
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"Crystal structure of Thermus aquaticus DNA polymerase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Thermus/Deinococcus group; Deinococci; Thermales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLA OR POL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                                                                                K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF
                                                                                                                                                                      Nature 382:278-281(1996).
                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96016150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 290-832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 376:612-616(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95364959; PubMed=7637814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89197950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermaceae; Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Overproduction of Thermus aquaticus DNA polymerase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishino Y., Ueno T., Miyagi M., Uemori T., Imamura M., Tsunasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         677 LSGELSIPYEE 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ructural analysis by ion-spray mass Biochem. 116:1019-1024(1994).
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                                                                                                                                                                                                                                                                                                                                         Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.C., Stoffel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17, created)
17, Last sequence update)
41, Last annotation update)
thermostable (BC 2.7.7.7) (Tag polymerase 1).
                                                                                                                                                                                             polymerase with DNA at the polymerase active site.";
                                                                                                                                                                                                                                                                                                                                      Sci. U.S.A. 92:9264-9268(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=7568114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2649500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saiki R.K., Myambo K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spectrometry."
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                                                                                                                   295-832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 831;
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EMBL;
PIR; A
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MEDLINE-99380545; PubMed=10449720;

Li Y., Mitaxov V., Waksman G.;

"Structure-based design of Taq DNA polymerases with improved properties of dideoxynucleotide incorporation.";

Proc. Natl. Acad. Sci. U.S.A. 96:9491-9496(1999).

-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS). MEDLINE=98445410; PubMed=9770525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase I complexed with deoxyribonucleoside triphosphates.", Protein Sci. 7:1116-1123(1998).
                                                                                                                                      Pfam; PF01367; 5_3_exonuclease; 1. Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                             BCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dynamics of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murali R., Sharkey D.J., Daiss J.L., Murthy H.M.K.; "Crystal structure of "Taq DNA polymerase in complex with an inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I: structural basis for nucleotide incorporation.";
EMBO J. 17:7514-7525(1998).
                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                         ; add
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fab: the Fab is directed against an intermediate in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structures of the Klenow fragment of Thermus aquaticus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98266352; PubMed=9605316;
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                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOTECHNOLOGY: Used in the PCR method because of its high thermostability. Has a relatively high error rate because it lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + [DNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exonuclease proofreading functionality
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                                                                                                                                                                                                                                                                         1QTM;
                                                                                                                                                                                                                                                                                                                                                                          3KTQ;
                                                                                                                                                                                                                                                                                                                                                            4KTQ;
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                                                                                                                                                                   PF00476; DNA_pol_A;
                                                                                                                                                                                  1РК003584; ЫНН_2
                                                                                                                                                                                                                                           IPR001098;
                                                                                                                                                                                                                                                          IPR002421;
                                                                                                                                                                                                                                                                                    30 SEP 98.
14 OCT 98.
12-MAR-97.
16-AUG-99.
16-AUG-99.
                                                                                                                                                                                                                                                                                                                                             08-NOV-96.
22-DEC-99.
22-DEC-99.
22-DEC-99.
22-DEC-99.
                                                                                                                                                                                                                 IPR000513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
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TIGREAMS; TIGRO0593; pola; 1.

PROSITE; PS00447; DNA\_POLYMERASE\_A; 1.

Transferase; DNA-directed DNA-polymerase; DNA replication; DNA-binding; 3D-structure.

POLYMERASE (BY SIMILARITY).

SMART; SM00475; 53EXOc; 1. SMART; SM00278; HhH1; 1.

SM00482; POLAC; SM00279; HhH2; PRINTS; PR00868;

DNAPOLI

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                                                           Pfam; PF00476; DNA_Pol_A; 1.
Pfam; PF0137; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuclease; 1.
Pfam; PF02739; 5_3_exonuclease; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THECA
                      TIGRFAMS; TIGR00593; pola; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                       or send an email to license@ish-sib.ch).
                                                                                                                                                                                                                                                                                                    entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                + {DNA}(N).
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93285135; PubMed=8508785; Park J.H., Kim J.S., Kwon S.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-GK24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kwon S.-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=GK24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I, thermostable (EC 2.7.7.7) (TAC polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993
01-NOV-1997
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           Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
                                                 SMART; SM00482; POLAC;
                                                                                                                                                                                                                                                PIR; $33287; $33287.
                                                                                                                                                                                                                                                              EMBL; U62584; AAB81398.1; -.
                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                       - I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_Tax1D=272;
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                                                                                                                                                         InterPro;
                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and characterization of Thermus caldophilus GK24 DNA
                                                                                                                                                                      InterPro;
                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 214:135-140(1993).
FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE ACTIVITY.
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                                                                                                                                                                                                                                     P19821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                      IPR003583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermus/Deinococcus group; Deinococci; Thermales
                                                                                                                                                                                                           IPR001098;
                                                                                                                                                         IPR003584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26, Created)
35, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 YW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%;
81.8%;
                                                                                                                                                                    EXO_N_I.
                                                                                                                                                         HHH_2
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                                                                                                                                                                                                       DNA_pol
                                                                                                                                                                                                                        5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park J.H., Kim H., Lee D.-S.;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F1731055B5246F03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee D. -S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        834 AA
                                                                                                                                                                                                                                                                                                                                            There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 832;
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                                                                                                                                                                                                                                                                                                                               is in
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Query Match
Best Local Similarity
Thinks 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
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                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase gene (polA) from Thermus thermophilus HB8.";
J. Ferment. Bioeng. 76:265-269(1993).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                         SMART; SM00279; HhH2; 1
SMART; SM00482; POLAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last annotation update) DNA polymerase 1, thermostable (RC 2.7.7.7) (Tth polymerase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                       SEQUENCE
                                                                                                 Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding.
                                                                                                                                                                                                                              Pfam; PF01367; 5_3_exonuclease; 1. Pfam; PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; D28878; BAA06033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to licensewisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urabe I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asakura K., Komatsubara H., Soga S., Yomo T., Oka M., Emi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPOT_THETH
                                                                                                                                PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                    SMART; SM00278; HhII1;
                                                                                                                                                                                                     SMART; SM00475; 53EXOc;
                                                                                                                                                                                                                   PRINTS; PR00868; UNAPOLI
                                                                                                                                                                                                                                                                           InterPro; IPR003584; HHLZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                            rlGRFAMs; TiGR00593; pola; 1.
                                                                                                                                                                                                                                                                                         InterPro; 1PR003583;
                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, nucleotide sequence, and expression in Escherichia coli of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              680 LSQELAIPYEE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                            PF00476; DNA_POI_A; 1.
                                                                                                                                                                                                                                                                                                                                                                  P19821; 1TAQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [DNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit
                                                                     834 AA;
                                                                                                                                                                                                                                                                                                        11/8000513;
                                                                                                                                                                                                                                                                                                                     IPRO02258; DNA Poli.
                                                                                                                                                                                                                                                                                                                                IPR001098; DNA_pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412
             Conservative
                                                                                      412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                     834
                                                                       94049 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       institutions as long as its content is
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                          81.8%;
                          90.0%; Score 45; DB 1; 81.8%; Pred. No. 0.3;
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                                                                     POLYMERASE (BY SIMILARITY)
; 1A98145DClla54A9 CRC64;
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Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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             Mismatches
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                                        Length 834;
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1 LSXFLSIPYEE 11

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RESULT 6
CIW5_HUMAN
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DT 16-CCT
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                                                                                                                                                                                                                                               CIW5_HUMAN
095279;
                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel channel protein TASK-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latteille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P38794;
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; SaccharomyceLes;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                             Homo sapiens (Human)
                                                                KCNK5 OR TASK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00385; CYCLIN; 1. PROSITE; PS00292; CYCLINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00134; cyclin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities re lires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCL5 OR YHR071W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G1/S-specific cyclin PCL5
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an cail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                   174 LNYELAIPYDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 LSQELAIPYEE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARTY: BELONGS TO THE CYCLIN FAMILY. MOST SIMILAR TO G1/S-SPECIFIC CYCLINS PCL# AND PCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMB1. outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S0001113; PCL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S46696; S46696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 31, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 31, Created)
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                                                                                                                                                                                                                                                                                  STANDARD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B6839ABB9DB5DD49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                               499 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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DE DI DAC
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                                                                                                                            POLG_OMV
                                                                                                                                           RESULT
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Best Local S
Matches
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Nuclear inclusion protein A (NI-A) (NIA)
(MC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99030343; PubMed=9812978;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF084830; AAC79458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                           P20234;
                                                                                                            POLG_OMV
                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and expression of a novel pH-sensitive two pore domain K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003280; K+channel_2pore
                                                                                                                                                                                          478 ELSVPYEQ 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                onic channel; "Transmembrane; ton transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lycoprotein
                                                                                                                                                                                                                         4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICIT: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
TISSUE SPECIFICIT: ABUNDANI, INTESTINE, IN THE KIDNEY, EXPRESSION
IN LIVER, PLACENTA AND SMALL INTESTINE, IN THE KIDNEY, EXPRESSION
IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 273:30863-30869(1998).
FUNCTION: PH DEPENDENT, VOLFAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACIDIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K+ CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:6280; KCNK5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . from human kidney
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR01333;
                                                                                                                                                                                                                                                                                                                      499 AA;
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  85
113
                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ion_trans;
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZFOREKCHANEL.
                                                                                                                                                                                                                                                                                                                                       26
112
133
157
157
180
215
250
325
                                                                                                                                                                                                                                                                                                                      55130 MW;
                                                                                                                                                                                                                                                                    74.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kichannel_pore.
                                                                                                                                                                                                                                                                                     Score 37;
                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                    PORE: FORMING 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PORE-FORMING 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                          PRT';
                                                                                                                                                                                                                                                                                                                      E871A7A4823DDA00 CRC64;
                                                                                                                                                                                                                                                        Mismatches
                                                                                                          1136
                                                                                                                                                                                                                                                                                     DB 1; Length 499
                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                         VE6_HPV31
                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                         P17386;
01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
15-JUN-2002 (Rel. 4
Human papillomavirus type 31.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00767; Poty_coat; 1.
Pfam; PF00863; Peptidase_C4; 1.
Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burger J.T., Brand R.J., Rybicki E.P.;
Burger J.T., Brand R.J., Rybicki E.P.;
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

Sibmitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.

1: FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

1: CATALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1'

that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tya-Xaa-

that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tya-Xaa-

The control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                              VE6_HPV31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coat protein; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D00615; BAA00490.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein (CP)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001730; Peptidase_C4.
InterPro; IPR001592; Poty_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS;
                                                                                                                                                                                                                                                                                                                                                                        698 KLSIPYEE 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity tes 7; Conserv
                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JQ0494; JQ0494.
PS; C04.005; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001205; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                            15, Created)
15, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365
883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128914 MW; 0A7AE0527743FD61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR INCLUSION PROTEIN A NUCLEAR INCLUSION PROTEIN B
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                              149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
THI4_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hest Local Similarity 63.68; Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on use by non-prolit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus.";
Virology 171:306-311(1989).
                                                                                                                                                            "Pyrithiamine resistance gene (ptrA) of Aspergillus oryzae: cloning, characterization and application as a dominant selectable marker for transformation.";
                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Thiazote biosynthetic enzyme, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZN_FING
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                          Biosci. Biotechnol. Biochem. 64:1416-1421(2000) -!- FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ezuueg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A32444; W6WL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDED DNA (IN VITRO).
                                                                        -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
                                                                                                                                                                                                          Kubodera T., Yamashita N., Nishimura A.;
                                                                                                                                                                                                                            MEDI.INE=20399355; PubMed=10945258;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID-5062;
                                                                                                                                                                                                                                                                                                             Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzac
                                                                                                                                                                                                                                                                                                                                                                  THIA OR PTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THI4_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Early protein; DNA-binding; Nuclear protein; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam; PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J04353; AAA46950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldsborough M.D., Disilvestre D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89299478; PubMed=2545036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LSSALEIPYDE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LSXELSIPYEE 11
                                                                                                            THIAZOLE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17713 MW; 61D2A86C362767D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 149;
                                                                                                                            THIAMINE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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the European Bioinformatics Institute.

non-profit institutions as long as its content is

There are no

restrictions on

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TREE REPORTED TO THE COMMENT OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Mouse;
MEDLINE=91319778; PubMed=1862107;
Korner J., Chun J., Harter D., Axel R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Reconvertase 1 precursor (EC 3.4.21.93) (NEC 1) (PC1)
(Prohormone convertase 1) (Proprotein convertase 1) (PC3) (Furin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD.
TRANSIT
1
2
MITOCHONDRION (POTENTIAL).
CHAIN
2
327
SEQUENCE
327
AA; 35099 MW; 7C561EE06742B2AE CRC64;
"Identification of a cDNA encoding a second putative prohormone convertase related to PC2 in AtT20 cells and islets of Langerhans.";
                                                                                                                                                                                                                                          "Cloning and primary sequence of a mouse candidate prohormone convertase PC1 homologous to PC2, Furin, and Kex2: distinct chromosomal localization and messenger RNA distribution in brach-
                                                                                                                                                                                                                                                                                                                           MEDLINE=91203919; PubMed=2017186;
Seidah N.G., Marcinkiewicz M., Benjannet
Mattei M.-G., Lazure C., Mbikay M., Chret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and functional expression of a mammalian processing enzyme, murine prohormone convertase 1.", Proc. Natl. Acad. Sci. U.S.A. 88:6834-6838(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCSK1 OR NEC1 OR NEC-1 OR Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P21662; P22546;
01-MAY-1991 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF217503; AAF25444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    MEDIINE=91110525; PubMed=1988934; Smeekens S.P., Avruch A.S., Lamendola J., Chan S.J., Steiner D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus cookii (Cook's mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEC1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS;
                                                                                                             SPECIES=M.cookii;
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                         pituitary compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakayama K., Hosaka M., Hatsuzawa K., Murakami K.;
"Cloning and functional expression of a novel endoprolease involved
in probormone processing at dibasic sites.";
J. Biochem. 109:803-806(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92041727; PubMed=1657897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELGVPYEE 145
                                                                                                                                                                                              Endocrinol.
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AMS; TIGR00292; Thi4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Propeptide processing protease).
NEC1 OR NEC-1 OR ATT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-LAF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                            ed to PC2.";
5:111-122(1991).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                         Chretien M.
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                                                                                                                                                                                                                                                                                                                                                                 s.,
                                                                                                                                                                                                                                                                                                                                                              Gaspar
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                                                                                                                                                                                                                                                                                                                                                                 Beaubien
                                                                                                                                                                                                                                                   brain
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Query Match
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EMBL; X57088; CAAA0368.1; P
EMBL; M5589; AAA39894.1;
EMBL; M55668; AAA39375.1; P
EMBL; M59196; AAA39732.1;
                                                   CARBOHYD
CONFLICT
                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seidah N.G.,
Chretien M.;
                                                                                                                                                           PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. [5]
                                                                                                                                                                                                          Prodom; PD000717; P_domain; 1.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS\text{-PROT} entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Release of protein hormones, neuropeptides and
renin from their precursors, generally by cleavage of -Lys-Arg-I-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chretien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cDNA sequence of two distinct pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE~91000356; PubMed~2169760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 214-478 FROM
                                                                                                                                                                                                                                                                                                                                                                         PIR; JX0171; KXMSC1.
PIR; A37951; A37951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS AT SITES COMPRISED OF PAIRS OF BASIC AMINO ACID RESIDUES. SUBSTRATES INCLUDE POWC, RENIN, ENREPHALIN, DYNORPHIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Cell Biol. 9:789-789(1990)
                                       SEQUENCE
                                                                           CARBOHYD
                                                                                                                                 DOMAIN
                                                                                                                                                DOMAIN
                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                   PRINTS; PR00723; SUBTILISIN
                                                                                                                                                                                                                                                                                Plam; PF01483; P; PARTIAL
                                                                                                                                                                                                                                                                                                         InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR002884; P_domain.
                                                                                                                                                                                                                                                                                                                                     MGD; MGI:97511; Pcsk1.
                                                                                                                                                                                                                                                                                                                                                 MEROPS; S08.072;
                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: LOCALIZED IN THE SECRETION GRANULES. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 furin gene products: tissue-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro-hormone
                                                                                                                                                                                                                                                                                                                                                               Q45670; 1DBI.
                                                                                                                                                                                                                                                                                             PF00082; Peptidase_S8;
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                                                                                                                                                                                                   Serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e processing proteinases.";
9:415-424(1990).
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POTENTIAL.
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N-LINKED (GLCNAC. . .)
S -> N (IN REF. 2 AND )
                                                                                       CHARGE RELAY SYSTEM (BY SIMILARITY) CHARGE RELAY SYSTEM (BY SIMILARITY) CHARGE RELAY SYSTEM (BY SIMILARITY)
           Score 36;
                                                                                                                                             CATALYTIC
                                                                                                                                 AMPHIPATHIC (POTENTIAL).
                                                                                                                                                           NEUROENDOCRINE CONVERTASE
                                                                                                                                                                        POTENTIAL
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                                       95B78441BE8BD9CD
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                                                                                                                                                                                                Zymogen; Calcium;
            Length 753;
                                       CRC64;
                                                 .) (POTENTIAL)
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                                                                             (POTENTIAL)
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Best Local Similarity
Matches 7; Conserv

Conservative

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RESULT 12
NEC1_RAT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Mitochondrial 60S ribosomal protein L8 (YML8).
                                                                                                                                                                                                Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-95282514; PubMed-7762302; Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.; "Sequence of a 17.1 kb DNA fragment from chromosome X of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRPL8 OR YJL063C OR J1125 OR HRD238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P22353;
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                             TIGRFAMS;
                                                                                                                                                                                                                                                          ProDom; PD004277;
                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of nuclear genes for two mitochondrial ribosomal proteins in Saccharomyces cerevisiae."; Nucleic Acids Res. 18:1521-1529(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RM08_YEAST
                                                                                                                                                                                                                                PROSITE; PS01167; RIBOSOMAL_L17; 1.
                                                                                                                                                                                                                                                                          Pfam; PF01196; Ribosomal_L17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 11:57-60(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90221879; PubMed=2183197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                             193 LLKEMSLPYDE 203
                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 SAKLSIPYE 698
                                                                                        1 LSXELSIPYEE 11
                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                       $14890; $14890.
$47128; $47128.
                                                                                                                                                                                                                                                                                                         S0003599; MRPL8
                                                                                                                                                                                                                                                                                                                                                 X53841; CAA37834.1; -. Z34288; CAA84050.1; -. Z49338; CAA89354.1; -.
                                                                                                                       Similarity
6; Conser
                                                                                                                                                                                                                                                                                        IPR000456; Ribosomal_L17.
                                                                                                                                                                                                                                             TIGR00059; L17;
                                                                                                                                                                                 238 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grohmann L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                           Ribosomal_L17; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19, Created)
                                                                                                                                                                                    26945 MW;
                                                                                                                                      54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graack H.-R., Isono K.;
                                                                                                                       ω,
                                                                                                                                       Pred. No. 8;
                                                                                                                                                    Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                   A130EFD95E8719BA CRC64;
                                                                                                                         Mismatches
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                                                                                                                                                    DB 1; Length 238;
                                                                                                                       2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
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CARBOHYD
                                                       ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences and the specific localization of each transcript to endocrine and neuroendocrine tissues in rats."; Endocrinoty 129:3053-305(1991)
-!- FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M76705; AAA4U945.1; EMBL; M83745; AAA41476.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manumalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Kattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                         CARBOHYD
                                                                                                       DOMAIN
                                                                                                                                                                                                                                                  PRINTS; PR00723; SUBTILISIN. Probom; PD000717; P_domain; 1
                                                                                                                                                                                                                                                                                   Pfam; PF00082; Peptidase_S8; Pfam; PF01483; P; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                      MEROPS; S08.072
                                                                                                                                                                                                                                                                                                                                                                                  PIR; A41556; KXRTC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hakes D.J., Birch N.P., Mezey A., Dixon J.E.; "Isolation of two complementary deoxyribonucleic acid clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92063860; PubMed=1954888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prohormone-converting enzymes: regulation and evaluation using antisense RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Prohormone convertase 1) (Proprotein convertase 1). PCSK1 OR NEC1 OR NEC-1 OR BDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroendocrine convertase 1 precursor (EC 3.4.21.93) (NEC 1) (PC1)
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                                                                                                                         DOMAIN
                                                                                                                                        CHAIN
                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                    PROSITE; PS00136; SUBTILASE_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat insulinoma cell line based on similarities to Kex2 and furin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92168040; PubMed~1791845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P28840;
                                                                                                                                                                                                                                                                                                                InterPro; IPR000209; Peptidase_S8
                                                                                                                                                                                                                                                                                                                                   interPro; IPR002884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloomquist B.T., Kipper B.A., Mains R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: LOCALIZED IN THE SECRETION GRANULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Release of protein hormones, neuropeptides and remin from their precursors, generally by cleavage of -Lys-Arg-[-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: CALCIUM DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOMATOSTATIN AND INSULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: INVOLVED IN THE PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS AT SITES COMPRISED OF PAIRS OF BASIC AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESIDUES. SUBSTRATES INCLUDE POMC, RENIN, ENKEPHALIN, DYNORPHIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinol. 5:2014-2024(1991).
                                                                                                                                                                                                                                                                                                                                                                    Q45670;
                                                                                                                                                                                                       PS00138;
                                                                                                                                                                                                                      PS00137;
                                                                                                                                                                                     Serine
        28
111
122
739
767
208
382
173
401
645
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                                                                                                                                                                                                   SUBTILASE_HIS; 1.
SUBTILASE_SER; 1.
                                                                                                                                                                                     protease;
                                                                                                                                                                                                                                                                                                                                     P_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
                                                                                                                                                                                    Glycoprotein; Zymogen; Calcium;
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                        CHARGE RELAY
                                                                                                      AMPHIPATHIC (POTENTIAL)
                                                                                                                     CATALYTIC
                                                                                                                                     NEUROENDOCRINE CONVERTASE 1.
                                                                                                                                                      POTENTIAL
                                                                                                                                                                    POTENTIAL.
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                                                                                    SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gutman P.D., Fuchs P., Ouyang L., Minton K.W.;
"Identification, sequencing, and targeted mutagenesis of a DNA polymerase gene required for the extreme radioresistance of Deinococcus radiodurans.";
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase I (EC 2.7.7.7) (POL I).
POLA OR DR1707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEIRA
                                                                                                       HSSP; P19821
TIGR; DR1707
                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996
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                                                      InterPro;
                                                                                InterPro;
                                                                                                                                                              EMBL; AE002012;
                                                                                                                                                                                     EMBL; L14581; AAC36974.1; -.
                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93273728; PubMed=8501062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 SAKLSVPYE 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Bacteriol. 175:3581-3590(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {DNA}(N)
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                                                                                                                                 19821; 2KTQ.
  IPR000513;
                                                   IPR002421;
IPR001098;
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514
752 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                              AAF11264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34, Created)
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514
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DNA_poli.
Exo_N_I.
                                                                                                                                                                                                                                                                                                                          institutions as long as its content
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                                                 DNA_pol
                                                                          5_3_exonuclease.
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E -> A (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group; Deinococci; Deinococcales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 AA.
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                                                                                                                                                                                                                                                                                                Usage
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase: DNA-directed DNA polymerase: DNA replication: DNA repair: Injurolase: Exonuclease: DNA-binding: Complete proteome. CONFLICT 48 48 T -> A (IN REF. 1).

CONFLICT 77 77 H -> D (IN REF. 1).

CONFLICT 108 108 F -> I. (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00476; DNA_pol_A; 1.
Pfam; PF01367; 5_3_exonuclease;
Pfam; PF02739; 5_3_exonuc_N; 1.
Yeast
                         Saccharomyces cerevisiae."; Yeast 10:481-490(1994).
                                                                 MEDLINE-95028146; PubMed-7941734; Praekelt U.M., Byrne K.L., Meacock P.A.; Praekelt u.M., Byrne K.L., Meacock P.A.; "Regulation of TH14 (MOLJ), a thiamine-biosynthetic gene of
                                                                                                                                                                                                      Skala J., Nawrocki A., Goffeau A.;
"The sequence of a 27 kb segment on the right arm of chromosome VII from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, CYS-PEMI/CHO2, MSR1 genes and ten new open reading frames.";
Yeast 11:1421-1427(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla
Nawrocki A., del Bino S., Goffean A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last annotation update)
Thiazole biosynthetic enzyme, mitochondrial precursor.
THI4 OR MOL1 OR ESP35 OR YGK144W OR G6620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993
01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00279; HhH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00475; 53EXOC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00868; DNAPOLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Praekelt U.M., Meacock P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryola; Fungl; Ascomycola; Saccharomycot:::::: Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P32318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                           MEDLINE-96158062; PubMed-8585325;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 205-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MOLL, a Saccharomyces cerevisiae quae that is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDI.INE=93070608; PubMed=1441749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THI4_YEAST
                                                                                                                                                        THIAMINE REGULATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  early stationary phase during growth on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 27, Created)
(Rel. 27, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
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L -> V (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6АННF117D75AB84A CRC64;
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Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirhness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                        STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
01-NOV-1997
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Q57567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Machado C.R., Praekelt U.M., de Oliveira R.C., Barbosa A.C.,
Byrne K.L., Meacock P.A., Menck C.F.;
"Dual role for the yeast THI4 gene in thiamine biosynthesis and DNA
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein MJ0103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thiamine biosynthesis; Mitochondrion; Transit peptide; FAD; NAD.
TRANSIT 1 MITOCHONDRION (POTENTIAL).
CHAIN 7 326 THIAZOLE BIOSYNTHETIC ENZYME.
NP_BIND 67 97 FAD OR NAD (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                              Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ELEIPYED 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01946; Thi4; 1.*
TIGRFAMs; TIGR00292; Thi4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0003376; THI4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S17019; S17019.
PIR; S25321; S25321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98035046; PubMed=9367751,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION IN DNA DAMAGE TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002922; Thi4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Mitochondrial (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: REPRESSED BY THIAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOLERANCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHASE OF BATCH CULTURES GROWING ON MCLASSES, AN INDUSTRIAL MEDIUM.
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35, Last seq
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75.0%;
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Pred. No.
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Search completed: January 15, Job time: 8.28572 secs
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the Buropean Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
-I- SIMILARITY: BELONGS TO THE UPF0063 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n_enk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                          Hypothetical protein; Complete proteome. SEQUENCE 433 AA; 49866 MW; F82576531DF12142 CRC64;
                                                                                                                                                                                                                                              InterPro; iPR000385; MoaA_NifB_PqqE.
Pfam; PF01444; MoaA_NifB_PqqE; 1.
                                                                                                                                                                                                                                                                                   TIGE; MJ0103;
                                                                                                                                                                                                                                                                                                EMBL; U67467; AAH98083.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                      33 EVEIPYEE 40
                                                                                                                                                            Local
                                                                                                        4 ELSIPYEE 11
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                                                                                                                                                                                                                                                                                                                  Score
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_unclassified:*
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5 Q9A3W3
094849
1 Q8VEI0
2 Q9YMM5
Q8TC35
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Q94248
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 Q8svp8 encephalito
Q49528 arabidopsis
Q9a3w3 caulobacter
Q94849 drosophila
Q8vei0 mus musculu
Q9ymm5 lymantria d
Q8tc35 homo sapien
                                                                                                                                                                 066691 aquifex aeo Q8u621 agrobacteri Q989f3 rhizobium 1 Q994W5 ornithogalu Q9jk62 mus musculu
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Q96IZ4	Q9NWW6	Q8Y3I4	Q926Q7	Q9ZQG2	P72904	Q9NFS3	Q917U4	Q24690	Q24363	P97528	88WF60	Q90Q52	Q8TJQ4	059717	Q9F"FX2	Q8:1:1S8	Q9V1T1	Q8Y7Q5	Q92СЛ1	Q9N610	Q9UXI2	Q8YAQ3	Q92FP6	Q92IY9	Q55139	Q58791	Q62845	Q9XWY5
Q96iz4 homo sapien	9nww6 homo	list	Q926q7 listeria in	Q9zqg2 arabidopsis	P72904 synechocyst	Ω	Q9i7u4 drosophila	690	Q24363 drosophila	752	Q9jmb8 mus musculu	Q9uq52 homo sapien	1 meth		tx2		_	Q8y7q5 listeria mo	<b></b>	Q9n610 leishmania	Q9uxi2 sulfolobus	Q8yaq3 listeria mo			Q55139 synechocyst	Q58791 methanococc	Q62845 rattus norv	Q9xwy5 caenorhabdi

## ALIGNMENTS

1451 AA

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Query Match
Best Local Similarity
Matches 7; Conserv
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Q9X148; O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last seque
O1-UN-2002 (TrEMBLrel. 21, Last annot
P91.1.15 protein.
                                                                                                                                                                                                                                                                                                                  STRAIN-CV. (SHIMBIA:

VYSOLSKAIA V.S., Schwattz J.R., Yu G., Tollumi M., Lenz C., Liu S.,

VYSOLSKAIA V.S., Schwattz J.R., Yu G., Tollumi M., Lenz C., Liu S.,

Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,

Altafi H., Araujo K., Brooks S., Bhuchler E., Chao Q., Conn L.,

Conway A.B., Dunn P., Hansen N., Hulzar L., Khan S., Kim C., Palm C.,

Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,

Pederspiel N.A., Theologis A.;

Pederspiel N.A., Theologis A.;

Parabidopsis thaliana chromosome 1 BAC F9L1 sequence.";

Submitted (JUN-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007591; AAD39650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryola; Viridiplanlae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                     SEQUENCE
                                                                                                                                          ATP-binding
                                                                                                                                                                        SMART; SM00382; AAA; 1.
                                                                                                                                                                                                      Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transportr;
                                                                                                                                                                                                                                                               InterPro; IPR003439; ABC_transportr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
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Conservative
                                 80.0%;
                                                                                                                     163602 MW;
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Last annotation update)
                              Score 40;
Pred. No.
      Mismatches
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                                                         DB 10; Length 1451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi (Lyme
Nature 392:353-358(1998).
               aeolicus
                   "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.":
                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                        STRAIN-VF5
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                 Bacteria;
                                                                                                                                                                              Aquifex aeolicus
                                                                                                                                                                                                           Hypothetical protein AQ_367
                                                                                                                                                                                                                                                                    066691;
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                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                                                                                                                                                                                                           43 SLELSVPYKE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U43739; AAA85591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE001137; AAC66681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390:580-586(1997).
                                                                                                                                                                Aquificae; Aquificales; Aquificaceae; Aquifex.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease spirochete).
                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E8AFB112B121F3B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                     850 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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gQ1.

Matches Qy

Conservative

Mismatches

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Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chon L., Wood C.E., Almelda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Romero P., Gordon D., Raymond C., Rouse G., Saenphinmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Cordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nachon P., Tingey S.V., Tomb J.-F., Gordon M.P., Oison M.V.,
                                                                                                                                                                                                                           Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houniel K., Cordon J., Vaudin M., Iartchouk O., Epp A., Liu P., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TremBirel 21, 01-JUN-2002 (TremBirel 21, 01-JUN-2002 (TremBirel 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001633; EAL.
InterPro; IPR001936; GGDEF.
InterPro; IPR001935; Mitoch_carrier.
Pfam; PF00563; EAL; 1.
                                                                                                                                                         "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
                                                                                                      Complete proteome.
                                                                                                                     EMBL; AE009395; AAL45459.1; ALT_INIT. EMBL; AE008220; AAK88782.1; -.
                                                                                                                                                                                                                                                                                                                      MEDLINE-21608551; PubMed-11743194;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                              Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MELA OR ATU4665 OR AGR_L_436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-galactosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8U6Z1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8U6Z1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome. SEQUENCE 850 AA; 97669 MW; CO2DCEF91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS00215; MUTOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00990; GGDEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=176299;
                                                                                                                                                                                                              Cielo C.,
                                                                                                                                                                                                                                                                                                                                                                                                       "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 ISREMDVPYEE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                              Slater S.;
                                                                                       474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium
                                76.0%;
63.6%;
                                                                                     53483 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                              Score 38; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                     16C1085B5A12B21B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C02DCEF91DBCDEB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 AA.
                                                 DB 16; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                Mullin L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Best Local :
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0904W5 PRELIMINARY;
0904W5;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 21, L
01-JUN-2002 (TrEMBLrel. 21, L
Polyprotein (Fragment).
Ornithogalum mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuk Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takacuchi C., Yamada M., Tabata S.;
                                                                                                   InterPro: [PR001592; Poty_coat.
InterPro: [PR001205; RNA_Pol_P3D.
Pfam: PP00767; Poty_coat; 1.
Pfam: PF00680; RNA_dep_RNA_Pol; 1.
                                                                                                                                                                                                               Mackenzie A., Gibbs A.;
"Potyviruses in Australia.";
"Potyviruses in Australia.";
Submitted (NOV-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF203528; AAF22752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-galactosidase.
MLR6450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD006892; GH_4; 1.
PROSITE; PS01324; GLYCOSYL_HYDROL_F4; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q989F3
                                                      SEQUENCE
                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12204;
                                                                                                                                                                                                                                                                                                                                                                                                           Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02056; Glyco_hydro_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesorhizobium loti.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 LAHDLSLPYDE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŋ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LSXELSIPYEE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00732; GLHYDRLASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7:331-338(2000).
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                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                      ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51818 MW;
                                                      53264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%;
54.5%;
  74.0%; Score 37; DB 12; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18,
18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6C29F18157E4F6EC CRC64;
                                                        3D4B484C259FF636 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 7
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Matches 7; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     094248;
01-MAY-1999 (TrEMBLrel. 10, Creaceu, 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1907 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                094248;
                                                 Murphy L., Harris \upsilon.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional properties of mouse "ASK-2 potassium channel."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP359395; AAF68668.1; -.
EMBL; AP319542; AAG35055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roux J., Barhanin J.;
"Mouse two P domain potassium Channel TASK2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=129/SVJ; TISSUE~KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLITE).
01-OCT-2000 (TrEMBLITE).
01-JUN-2002 (TrEMBLITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9JK62;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JK62
                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                        Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                        SPCC737.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01333; 2POREKCHANEL Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003280; Kichannel_2pore.
InterPro; IPR001622; Kichannel_pore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1336175; Kenk5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cid L.P., Niemeyer M.l.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCNK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potassium channel TASK2 (TASK2 potassium channel).
STRAIN=972H-;
                        SEQUENCE FROM N.A.
                                                                                                                             STRAIN=972H-;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID-4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKELLMINAKY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55976 MW; E4C7E7CC71B4:075 CRC64;
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15, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                        Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sepulveda F.V.;
                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
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                                                                                                                                                                                                                                                                                    Schizosaccharomycetes;
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01-JUN-2002
01-JUN-2002
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Submitted
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01-JUN-2002 (TTEMBLrel. 21, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate
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InterPro; IPR002048: EF-hand.
InterPro; IPR002035; VWE_A.
Pfam; PF00004; AAA; 3.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter tengcongensis.

Bacteria; Firmicutes, Bačillus/Clostridium group; C
Thermoanaerobacteriales; Thermoanaerobacteriaceae;
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PROSITE; PS50234; VWFA; 1.
SEQUENCE 4717 AA; 537775 MW; B2BC
              SEQUENCE FROM N.A. STRAIN=GB-M1;
                                                               Eukaryota; Microsporidia;
NCBI_TaxID=6035;
                                                                                                                   Hypothetical protein ECU04_1610.
                                                                                                                                                                                                          Q8SVP8;
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Bao Q., Tian Y., Li W., Xu 2., Xuan Z., Hu S.,
Chen Y., Xu. Y., Lai X., Huang L., Dong
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome
Genome Res. 12:689-700(2002).
EMBL; AE013059; AAM24189.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
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                                                                                                     Encephalitozoon cuniculi.
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Genoscope;
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                                                                                                                                                                                                                                                                                                                        IARELNIPFEE 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 AA; 32346 MW;
                                                                                                                                  (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
1 protein ECU04_1610.
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63.6%;
                                                                                      Unikaryonidae;
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2; Mismatches
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105072D27AB06FFE CRC64;
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                                                                                      Encephalitozoon
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Ling L.,
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Submitted (MAR-2000) to the
EMBL; AL021710; CAA16740.1;
EMBL; AL161549; CAB78862.1;
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 206.8 kDa protein F28J12.260 in chromosome IV
                                                                                                                                                                                                                                                                             Hilbert H., Braun M., Holzer
Mewes H.W., Lemcke K., Mayer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bevan M., Hilbert H., Br. Bancroft I., Mewes H.W.,
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F28J12.260 OR AT4G18600
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                                                                                                                                     project;
Score 36; DB
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K., Schueller C.;
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            DB 10;
2.8e+02;
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Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF02798; GST_N; 1.
Pfam; PF02798; GST_N; 1.
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last seq.
01-JUN-2001 (TREMBLREL. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nolson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Eisen J., Heison W.C., Newton A., Stephens C., Phadke N.D., Ely B., Dotocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Hatt D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Wolfe A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Complete genome sequence of Caulobacter crescentus.*; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9A3W3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutathione S-transferase family protein.
              "Pattern of ecological shifts in the diversification of Hawailan Drosophila inferred from a molecular phylogeny.";
Curr. Biol. 5:1129-1139(1995).
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                                                                                                                                                                            Drosophila buzzatii (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                              Q94849
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                                                               Cohen J.;
                                                                             MEDLINE-96120851; PubMed-8548285;
Kambysellis M.P., Ho K.F., Craddock E.M., Piano F.,
                                                                                             MEDLINE=96120851;
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                                                                                                                                                                 Ephydroidea;
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70.0%;
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Pred. No. 44;
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RESULT 14
Q8VEIO
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                                                                                           MEDLINE-99124785; PubMed-9887315;
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Slavicek J.M., Rohrmann G.F.;
"Sequence and analysis of the genome of a baculovirus pathogenic for
Lymantria dispar.";
Virology 253:17-34(1999).
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Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
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01-MAY-1999 (TrEMBLTel, 10, Last seq
01-DEC-2001 (TrEMBLTel, 19, Last ann
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Mammalia; Eutheria;
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01-MAR-2002 (Tremblice).
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                           Nucleopolyhedrovirus.
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Post-processing: Minimum Match 08
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 5 from patent US 5466591
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           Sequence 2 from patent US AR023961
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Sequence 2 from patent US 5837450.
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Dahlberg, J.E., Lyami
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1 (bases 1 to 2496)
Brow, M. Ann. D., Hall, J. Steven. Grotelueschen., Lyamichev, V.,
Olive, D. Michael. and Prudent, J. Robert.
Detection of nucleic acid sequences by invader-directed cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2496)
Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 2 01-DEC-1998;
                                                                                                                                 Sequence 2 from patent US 5846717. AR063636
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Heisler, L.M., Fors, L
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                                                             Unclassified.
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                        Patent: US 5994069-A 2 30-NOV-1999;
                                      cleavages
                                                   Hali,J.G., Lyamichev,V.I., Mast,A.L. and Brow,M.Ann.D. Detection of nucleic acids by multiple sequential inva
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Prudent,J.R., Hall,J.G., Lyamichev,V.I., Brow,M.Ann.D. and
Dahlberg,J.E.
                                                                                                                                                          Unknown
                                                                                                                                                                                                               Sequence 2 from patent US 6348314.
AR193571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olive, D. Michael. and Prudent, J. Robert.

Detection of nucleic acid sequences by invader-directed cleavage Patent: US 6001567-A 2 14-DBC-1999;
                                                                    Invasive cleavage of nucleic acids Patent: US 6348314-A 2 19-FEB-2002;
                                                                                                                                           Unclassified.
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Brow, M. Ann. D., Hall, J. Steven. Grotelueschen., Lyamichov, V.,
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Sequence 154 from Patent Woo190337.
AX31715]
                                                                                Patent: WO 0190337-A 154 29-NOV-2001; THIRD WAVE TECHNOLOGIES, INC. (US)
                                                                                                                            Allawi, H., Bartholomay, C.T., Chehak, L., Curtis, M.L., Bis, P.S., Hall, J.G., Ip, H.S., Kaiser, M., Kwiatkowski, R.W., Lukowiak, A.A., Lyamichev, V. Ma, W., Olson, Munoz, M.C., Olson, S.M., Schaeler, J.J., Skrzypczynski, Z., Takova, T.Y., Vedvik, K.L. and Lyamichev, N.E.
                                                                                                                                                                                                                              Thermus thermophilus Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
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Dahlberg,J.E., Lyamichev,V.I. and Brow,M.Ann.D.
5' nucleases derived from thermostable DNA polymerase
Patent: US 5614402-A 2 25-MAR-1997;
Location/Qualifiers
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Sequence 2 from patent US 5541311.
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Sequence 2 from patent US 5614402.
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Dahlberg, J.E., Lyamichev, V.I. and Brow, M.Ann.D.
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                                                                                   Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAB47791-97 and AAM48259 AAM448270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase .
                           Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                               WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dye; amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Native DNA polymerase motif #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM48260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 4; 23pp; English
                                                                                                                                                                                                                                                                                                  Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                                                                                                                (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001; 2001EP-0109341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48260 standard; Peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in reverse transcription/amplification reactions. The method
                                                                                                                                                                                                                                                                                                                                 Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                  Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pieu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.0%;
                                                                                                                                                                                                                                                                                                                              Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                              Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 3
AAM48263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the RNA, a primer, a divalent cation, and a mutant thermoactive DNA.
                                                                                                                                                                               Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concentrations relative to previous high Lemperature reverse transcription methods, and provide a wider range of usable sait concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme
                                                                                                                                                                                                                                                    WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                    Schoenbrunner NJ,
                                                                                                                                                                                                                                                                                                 Smith BS, Blfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus species sps17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Native DNA polymerase motif #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48263 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase. These motifs represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                 (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              needed for the reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                    Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.0%;
90.9%;
                                                                                                                                                                                                                                                                                                 Gelfand DH,

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 23; Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                 Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DNA polymerase's ability to incorporate dideoxynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method

RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the

The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DAA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the

Disclosure; Page 7; 23pp; English.

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AAM48265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                        fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster
                                                                                                                                                                                                                                                native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                         RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxynucleotides labelled with
                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-198336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Native DNA polymerase motif #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM48265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM48265 standard; Peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse
                                       needed for the reaction.
                                                           reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                          The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 7; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus filiformis. ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               needed for the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schoenbrunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE & CO AG F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LSQELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elfstrom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 23;
Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Higuchi RG, Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Sequence

11 AA;

Query Match Best Local : Matches

10; Similarity

Conservative

0;

Mismatches

Indels

0;

Gaps

0;

96.08;

Score 48; DB 1 Pred. No. 0.45;

DB 13; Length 545;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.0%;
Best Local Similarity 90.9%;
                                                                                                    The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 288 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in bomogeneous assays for the amplification and detection of a larget mutant of a company of the polymerase light of the sustained sequence representation of a larget may be desirable in enzymes used in
                                                                                                                                                                                                                                                                                Claim 11; Page 59; 185pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant thermostable DNA polymerase enzyme MET-ALA 288 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR23157 standard; Protein; 545 AA
Sequence
                                                                                                                                                                                                                                                                                                                           Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus species SPS17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR23157;
                                                           regions of the enzymes can be used to prepare a range of recombin
proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ24010
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                        Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-0CT-1992 (first entry)
                               See also AAR23140-79 and AAR23722.
                                                                                          nucleic acid sequence.
                                                                                                                                                                                                                                                                                                            in e.g. PCk, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSQELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
   545 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9008-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0590213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "residues 2-287 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                       Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence"

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                           for use
                                                                           recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                  exonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 6
AAR23156
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                                                                        Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                     and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                             The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-THR 200 Tsps17, having a different amt. of 5'-3' exonucleas activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ24009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus species SPS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant thermostable DNA polymerase enzyme MET-THR 200 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR23156 standard; Protein; 632 AA
                                                                                                                                                              See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-d fc ence 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR23156;
                                                                                                                                                                                                                                                                                                                                                                                                                                  in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1992
               478 LSQELSIPYEE 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 LSQELSIPYEE 400
                                                                                       Local
                                           1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>د</u>ـــو
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSXELSIPYEE 11
                                                                        l Similarity
10; Conserv
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0590466.
90US-0590490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                    96.0%;
                                                                        0;
                                                                                    Score 48; DB 1
Pred. No. 0.53;
                                                                        Mismatches
                                                                                                    DB 13; Length 632;
                                                                        1; Indels
                                                                        0;
                                                                                                                                                                                                                                                                                                                                                       exonuclease
                                                                      Gaps
                                                                        0;
AAR23154
ID AAR2
                            RESULT 8
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AAR23155
ID AAR
XX
dd.
                            Qy
                                                                                                                       RESULT 7
                                                            Matches
                                                                         Best Local Similarity
                                                                                         Query Match
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28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                      may facilitate higher sensitivity allelic discrimination in a combined polymerase figure chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                              The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-LNU 152 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                           nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                 activity than the native enzyme. Thermostable DNA pare useful in many recombinant DNA techniques, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ24008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus species SPS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1992 (first entry)
                                                                                                                      Sequence
                                                                                                                                                   See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                  amplification by MCR, self sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity
                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase enzyme MET-LEU 152 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR23155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR23155 standard; Protein; 680 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1992
526 LSQELSIPYEE 536
                              1 LSXELSIPYEE 11
                                                            10;
                                                                                                                      680 AA;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9005-0590466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0590213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                       90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence"
                                                           0
                                                                       Score 48; I
Pred. No. 0.
                                                            Mismatches
                                                                                      DB 13; Length 680;
                                                                         .58;
                                                                                                                                                                                                                                                                                                                  nucleic
                                                           0,
                                                         Gaps
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AAR23154 standard; Protein; 758 AA

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AAR23153
ID AAR:
XX
AC AAR:
XX
DT 22-0
                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-ALA 74 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and high temp. DNA sequencing. The absence of 5'-3' nuclease activity and fighter sensitivity allelic discrimination in a combined
      22-OCT-1992 (first entry)
                                                      AAR23153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase ligase chain reaction (PLCR) assay. An enhanced amt. o. 5'-3' exonuclease activity may be desirable in enzymes used in homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable DNA polymerases with altered 5^{\prime}-3^{\prime} exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                          AAR23153 standard; Protein; 788 AA.
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence. Mutation of the DNA encoding particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ24007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant thermostable DNA polymerase enzyme MET-ALA 74 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                 See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus species SPS17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR23154;
                                                                                                                                                                                              604
                                                                                                                                                                                                                                   1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                              LSQELSIPYEE 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1992-150885/18
                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                            758 AA;
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0590213.
90US-0590466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "residues 2-73 deleted from the native
                                                                                                                                                                                                                                                                                               90.9%;
                                                                                                                                                                                                                                                                                                                   96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence"
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                               0.66;
                                                                                                                                                                                                                                                                                                                 DB 13; Length 758;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amt, of
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                          0;
        WX XX DT XX AC XX
                                                                                                                                                                                          RESULT 10
AAR23152
                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a mutant of Thermus species sps17 polymerase mutant MET-PHE 43 Tsps17, having a different amt, of 5'-3' exonucleas activity than the native enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, esp. nucleic acid
                                         Mutant thermostable DNA polymerase enzyme ASP43 Tsps17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence. Mulation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinant proteins having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus species SPS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant thermostable DNA polymerase enzyme MET-PHE 43 Tsps17.
                                                                                  22-OCT-1992 (first entry)
                                                                                                                               AAR23152;
                                                                                                                                                                  AAR23152 standard; Protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAR23140-79 and AAR23722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homogeneous assays for the amplification and detection of a target
                                                                                                                                                                                                                                                                          634 LSQELSIPYEE 644
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                              1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                     l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ24006
                                                                                                                                                                                                                                                                                                                                                                                                                                          788 AA;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0590490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-US07035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "residues 2-43 deleted from the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 13; Length 788; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                       . 0.69;
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exonuclease

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Indels

0; Caps

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RESULT 11
AAR76060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful in many recombinant DNA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5'-3' nuclease activity may facilitate higher sensitivity allelic discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' exonuclease activity may be desirable in enzymes used in 5'-3' ex
                      W09514770-A
                                                                                                                          DNA-polymerase; Ifil; thermostable enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to prepare a range of recombinations having 5'-3' exonuclease activity to a complete lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a mutant of Thermus species sps17 polymerase mutant ASP43 Tsps17, having a different amt. of 5'-3' exonuclease activity than the native enzyme. Thermostable DNA polymerases
                                                                        Thermus filiformis
                                                                                                                                                                         Tfil DNA-polymerase
                                                                                                                                                                                                                                   28-0CT-1995
                                                                                                                                                                                                                                                                                        AAR76060;
                                                                                                                                                                                                                                                                                                                                     AAR76060 standard; Protein; 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAR23140-79 and AAR23722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 59; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ24005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abramson RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9206200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in e.g. PCR, sequencing and detection assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-150885/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus species sps17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 LSQELSIPYEE 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gelfand DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0590213.
90US-0590466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0590490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-US07035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Gly in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 13; Length 830; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                              5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed enzyme) has reverse-transcriptase activity in the presence of Mg2+. The enzyme is a versatile DNA-polymerase suitable for use in DNA synthesis from DNA and RNA templates, and for automated DNA sequencing. Both of these reactions are performed in the same buffer. The enzyme has a high salt tolerance and is also suitable for use in cycled fluorescent
         Disclosure; Page 83-86; 159pp; English.
                                                                                                                                                                                                                                                                                                          DNA-polymerase; DNAP; Tfl; DNA cleavage; RNA cleavage; 5' nuclease
                                                                                                                                                                                                                                                                                                                                      T. flavus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                  AAR64273 standard; Protein; 831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing using dye-primers and dye-terminators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-206929/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1995.
                                                                                      N-PSDB; AAQ80750.
                                                                                                                           Brow MAD, Dahlberg JE,
                                                                                                                                                                                 04-JUN-1993;
                                                                                                                                                                                                          06-JUN-1994;
                                                                                                                                                                                                                                    22-DEC-1994
                                                                                                                                                                                                                                                             W09429482-A
                                                                                                                                                                                                                                                                                    Thermus flavus AT-62.
                                                                                                                                                                                                                                                                                                                                                                19-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                            AAR64273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New heat-stable DNA polymerase from Thermus filiformis - has reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ92369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bergquist PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PACI-) PACIFIC ENZYMES 1993 LTD
                                                                                                    WPI; 1995-036504/05
                                                                                                                                                      (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA-polymerase Tfil (DNA nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptase activity in the presence of magnesium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676 LSQELSIPYEE 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Day DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-NZ00135
                                                                                                                                                                                 93US-0073384.
                                                                                                                                                                                                          94WO-US06253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93NZ-0250288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibbs MD,
                                                                                                                           Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 16; Length 830; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reeves RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saul DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
for the detection of non-target cleavage products via the formation of a complete and activated protein binding region, and methods for the detection of nucleic acid from various viruses (e.g. human cytomegalovirus) in a sample. The method amplifies the detection molecule rather than the target itself, is less subject to contamination than exponential amplification processes, and allows many targets to be analysed in a single reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-polymerase (DNAP) are given in AAQ80750 and AAR64273, respectively. 5' Nucleases, such as those given in AAQ80742-45, derived from thermostable DNAPs show reduced synthetic activity whilst retaining structure-specific cleavage activity.
                                                                                                                                                                                                                                     and variations in nucleic acid sequences. It also relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving this structure in a site-specific manner,
                                                                                                                          AAV65783-86). Cleavage of the cleavage structure by the nuclease indicates the presence of specific nucleic acid sequences or specific variants. The invention further relates to methods for the separation of nucleic acid molecules based on charge, methods the separation of nucleic acid molecules based on charge, methods
                                                                                                                                                                                                  preferably using a thermostable structure-specific nuclease such as a modified Thermus DNAP that has reduced synthetic activity (see
                                                                                                                                                                                                                                                                                                                                                                                                   cytomegalovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting target nucleic acid by sequence-specific cleavage of complex with two specific oligonucleotides - used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV65780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9842873-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus flavus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW79961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW79961 standard; Protein; 831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA and amino acid sequences of T. flavus AT-62 thermostable
                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the thermostable DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 266-268; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid detection; multiple sequential invasive cleavage;
                                                                                                                                                                                                                                                                                        for the detection and characterisation of nucleic acid sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 LSGELSIPYEE 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1598-557036/47
                                                                                                                                                                                                                                                                                                           of Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0823516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US05809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kwiatkowski RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                           The invention relates to means
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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AAW80428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                      duplex structure to create a single, single-stranded cleavage product. The methods are used for the specific detection of nucleic acid sequences, via a cleavage-based procedure, but without the need for amplification of target sequences. Thermostable polymerases, altered to have nuclease, but not polymerase activity are preferably used due to their specificity. The cleavage product specifically formed is detected, preferably by the use of radioactively labelled oligonucleotides. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                 describes a method for detecting the presence of a nucleic acid molecule. The method uses a thermostable 5; nuclease derived from a thermostable polymerase modified to have reduced synthetic activity, where the 5; nuclease is capable of cleaving a linear nucleic acid
                                                                                                                                                                                                                                                                                                          Detection of target nucleic acid molecules - uses modified thermostable enzymes with specific cleavage activity to create specific detection products from oligo:nucleotide(s) and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable DNA polymerase; nucleic acid detection; thermostable 5' nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW80428 standard; Protein; 831 AA
                                                                                                                                                                                                                                                               Disclosure; Fig 3; 91pp; English.
                                                                                                                                                                                                                                                                                              hybridisation
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV63401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5837450-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW80428
                                                                                                                                                                                                               The present sequence represents a thermostable DNA polymerase enzyme. The sequence is used in the course of the invention. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17~NOV-1998
                        can be used in e.g. forensic testing or paternity determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   677 LSGELSIPYEE 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                        1999-023438/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             831 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0073384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0254359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0471066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-0986330
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Lyamichev VI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 1
Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                               The specification
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Query Match

Sequence

831 AA;

Matches

Local L.

Similarity

96.0%;

Score 48; DB 2 Pred. No. 0.73;

DB 20; Length 831;

0;

Mismatches

0;

Gaps

0;

δδ

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RESULT 15
AAR728
ID AAR72
XX AR72
XX D5-DEC
XX P01ym
XX P01ym
XX P01ym
XX P01ym
XX P1-AP
PR 11-AP
PR 12-AU
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Search completed: January 15, 2003, 11:20:16 Job time : 30.2857 secs
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Best Local S
Matches 10
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22-AUG-1986;
17-JUN-1987;
12-JAN-1988;
15-MAY-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the thermostable polymerase of Thermus species \operatorname{sps17}. The Gly residue at position 43 may be substituted for an Asp residue. This substitution is shown to result in a 100 fold decrease in the 5^{\prime}-3^{\prime} exonuclease activity with no change to the polymerase activity of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus species sps17.
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 7-12; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA for Thermus species sps17 DNA polymerase - modified to encode an N-terminal deletion to reduce 5'-3' exo:nuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ86927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-154582/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymerase; Thermus; enzyme; thermostable; exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsps17 polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abramson RD, Gelfand DH, Greenfield IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHÉ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1986;
                                                                                                                                691 LSQELSIPYEE 701
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                                                                                                                                                                                                                                          y Match 96.0%;
Local Similarity 90.9%;
hes 10; Conservative
                                                                                                                                                                 1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LSXELSIPYEE 11
                                                                                                                                                                                                                                                                                                                                                                          845 AA;
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86US-0899241.
87US-0063509.
88US-0143441.
90US-0523394.
90US-0590213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86US-0899241.
                                                                                                                                                                                                                                             Score 48; DB 16; Length 845; Pred. No. 0.74; O; Mismatches 1; Indels
                                                                                                                                                                                                                                                    0;
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OM protein - protein search, using sw model

GenCore version 5.1.3 Compute Copyright (c) 1993 - 2003 Copyright (c) 1993 -

Compugen Ltd

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P74299 synechocyst
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P49404 caenorhabdl
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haemophilus
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  aquifex aec
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RESULT 2
ANGT_RAT
ID ANGT
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DT 21-J
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                                                                                                                                                                                                                                        Matches
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Best Local
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01-NOV-1997
01-NOV-1997
P01015;
21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                            Pfam; PF01408; GF0_IDH_MOCA.C; 1.
Pfam; PF02894; GF0_IDH_MOCA.C; 1.
Hypothetical protein; Plasmid; Oxidoreductase; NAD.
NP_BIND 4 22 NAD (BY SIMILARITY).
                                           ANGT_RAT
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000583; GFO_IDH_MocA_C. InterPro; IPR004104; GFO_IDH_MocA_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to licensesisb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the FMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 387:394-401(1997).
-!- FUNCTION: COULD BE A NAD-DEPENDENT OXIDOREDUCTASE.
-!- SIMILARITY: LOW, TO R.MELILOTI RHIZOPINE CATABOLISM PROTEIN MOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid sym pNGR234a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y40X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 39.9 kDa protein Y40X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P55609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE0000089; AAB91810.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y40X_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perret X.
                                                                                                                                                   337 SVRLGQPVK 345
                                                                                                                                                                                          2 SVRLGXPVK 10
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8; Conserv
                                                                                                                                                                                                                                                                                                                         360 AA;
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(Rel. 35, Last seq
(Rel. 35, Last ann
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                                                                                                                                                                                                                                                       Score 38; DB 1; Length 360; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                       NAD (BY SIMILARITY). 59998F508ZDE26CA CRC64;
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ong as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercial
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Result

Score

Match

Length

B

SUMMARIES

77.6 73.5 73.5

YCXB\_PORPU

P55611 I-51234 P18650

APE\_PIG

RECA\_THEMA RM03\_CAEEL

YNHG\_ECOLI

P76193 Q9h583 Y40X\_RHISN

GGA1\_YEAST

HEAD\_BPPH8 RNFC\_BUCAI

PCL1\_ARATH

P05481 P57215 P57681 P74884 P33650

964 1034 12265 1226 1223 123 155 249 259 259 259 302 302 313 451 521 759 819

MURB\_HELPJ MURB\_HELPY

APX1\_PEA CHEW\_CAUCR GALA\_BOVIN DSRA\_HUMAN

P07480 087715 P48534 Q9zjj4 025963 P75836

0

YCAN\_ECOLI

P60\_LISGR
VP7\_WTV
PURL\_THEAC
RNFC\_HAEIN

Q10518 Q9jyz2 Q91835 Q01835 P13092 Q9hja4 P71397

COBD\_MYCTU EX7L\_NEIMB

CAPP\_SYNY3
RPC2\_SCHPO

FEOB

\_ECOLI

LON2\_MAIZE FEOB\_SALTY Minimum DB

Maximum DB

seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

SwissProt\_40:\*

and is derived by Pred. No. Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext

Perfect score:

US-09-823-649A-5 49

LSVRLGXPVKE 11

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δÃ
 B
                                                                                                                            Matches
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L00094; AAA98779.1; -
EMBL; L00091; AAA98779.1; JOINED.
EMBL; L00092; AAA98779.1; JOINED.
EMBL; L00093; AAA98779.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiotensin and its identification by DNS-method.";
Chem. Pharm. Bull. 20:1579-1581(1972).
-1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE,
                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83169849; PubMed=6572971;
Ohkubo H., Kageyama R., Ujihara M., Hirose T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Kattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensinogen precursor [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                            CARBOHYD
                                                                                                                                                             CARBOHYD
                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                             PEPTIDE
                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                         Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                       Pfam; PF00079; serpin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakayama T., Nakajima T., Sokabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=73060322; PubMed=4344907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000227; Angiotensngn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative studies on angiotensins.
 148
                                                                              Local
                                1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.
                                                                                                                                                                                                                                                                                                                                                                         A01251; ANRT
LQVLLGVPVKE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERPINA8
                                                                                                                                                                                                                                                                                          SM00093; SERPIN;
                                                               Similarity
8; Conser
                                                                                                                                                                                                                                                                                                         PR00654;
                                                                                                                                                                                                                                                                          PS00284;
                                                                                                                                                                                                                                                                                                                                      IPR000215; Serpin.
                                                                                                                           295
319
477 AA;
                                                               Conservative
                                                                                                                                                                                                                                                                                                         ANGIOTENSNON.
                                                                                                                                                                                                                                                                          SERPIN; FALSE_NEG
                                                                                                                            51981 MW;
                                                                           73.5%;
72.7%;
                                                               0;
                                                                              Score 36;
Pred. No.
                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
689051A5788D693D CRC64;
                                                                                                                                                                         ANGIOTENSIN II.
                                                                                                                                                                                                         ANGIOTENSINOGEN.
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb~sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II. Structure of rat
                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage by and for commercial
                                                               3; Indels
                                                                                          Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE ENZYME RENIN
                                                             0;
                                                               Gaps
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                                                                                                                 Matches
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Zamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9H583; Q9NN23;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Hioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (FiB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK001221; BAA91564.1; ALT_INIT INTERPRO; IPR000357; HEAT_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bougueleret I., Chumakov I., Barry C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein BAP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP28_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AX067150; CAC26776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 HEAT REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1777-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1534-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel BAP28 gene and protein.";
Patent number WOOl00669, 04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANTS S-1694; A-1854; D-1967 AND G-2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000357;
923 LLINLGSPVKE 933
                                                                                                                                          Local
                                                     1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL136105;
                                                                                                              l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                               2017
                                                                                                                                                                                                                                                                                                                                                           1967
                                                                                                                                                                                                                                                                                                                                                                                                                    1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1694
                                                                                                                                                                                                                                   2144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2106
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAC15948.1;
                                                                                                                                                                                                                                                                                               2017
                                                                                                                                                                                                                                                                                                                                                        1967
                                                                                                                                                                                                                                                                                                                                                                                                                 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1694
                                                                                                                                          63.6%;
                                                                                                                                                                                                                                   242355
                                                                                                                                                                       73.5%;
                                                                                                                                                                                                                                   WW;
                                                                                                                                                                 Score 36; DB 1; Length 2144;
                                                                                                        Pred. No. 31;
l; Mismatches
                                                                                                                                                                                                                                                            /FTId-VAR_010942
                                                                                                                                                                                                                                                                                                                     /FTId=VAR_010941
                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_010940
                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_010939
                                                                                                                                                                                                                                                                                                  v
G
                                                                                                                                                                                                                                D66816EE78D8C9B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen-Akenine A.;
                                                                                                              0;
                                                                                                           Gaps
                                                                                                              0;
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RESULT 4
YNHG\_ECOLI

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DI AC
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                                                                                                                                                                                                                                                                                                                                               RECA_THEMA
                                                                                                          RESULT
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                    Query Match
                                           RECA_THEMA
P36203;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002482; LysM.

Pfam; PP01476; LysM; 1.

SMART; SM00257; LysM; 1.

Hypothetical protein; Periplasmic; Signal; Complete proteome.

SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
    01-JUN-1994
                      01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0\text{-}40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D90811; BAA15458.1; -.
EMBL; D90812; BAA15464.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000263; AAC74748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWTSS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein ynhG precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG14015; ynhG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE ERFK/YBIS/YCFS/YNHG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto Y., Horiuchi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-233 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNHG OR B1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P76193; P76899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNHG_ECOLI
                                                                                                                                                                            223 SYRTGTPVK 231
                                                                                                                                                                                                                                                           Local Similarity es 7; Conser
                                                                                                                                                                                                                  2 SYRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. 3:363-377(1996).
SUBCELLULAR LOCATION: Periplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shao Y.;
                                                                                                                                                                                                                                                                                                                                            334 AA;
(Rel. 29, Created)
(Rel. 29, Last sequence update)
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P76900
                                                                                                                                                                                                                                                                                                                                               36082 MW;
                                                                                                                                                                                                                                                                               69.4%;
77.8%;
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                 Score 34;
                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN YNHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                               25078BB429389D5F CRC64;
                                                                                                                                                                                                                                                             Mismatches
                                                                 356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 AA
                                                                                                                                                                                                                                                                                                    DB 1; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation -
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                             SOUCH AND THE REAL BREAK BREAK
  RM03_CAEEL
ID RM03_0
                                                                                                        ₽
                                                                                                                                              Ş
                                           RESULT 6
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                  Best
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Query Match
   RM03_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Hait D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Stewart A.M., Sutton G.G., Fleischmann R.D., Elsen J.A., White O., Salzberg J.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- FUNCTION: CAN CATALYZE THE HYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 269:25928-25935(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-95014407; PubMed=7929298; Wetmur J.G., Wong D.M., Ortiz B., Tong J., Reichert F., Gelfand D.H.; Wetmur J.G., Wong D.M., Ortiz B., Tong J., Reichert F., Gelfand D.H.; "Cloning, sequencing, and expression of RecA proteins from three distantly related thermophilic eubacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. NP_BIND 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001823; AAD36921.1; -. HSSP; P26345; 1G19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L23425; AAA27417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statcment is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermotogae; Thermotogae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECA OR TM1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reca protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00154; recA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; AAA_ATPase
InterPro; IPR001553; RecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; TM1859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                       225 MEVRRGEPIKE 235
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                 1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAS. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE RECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD000229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00142; RECA.
                                                                                                                                                                                                                                                                                                                                                                                                  356 AA;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / DSM 3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Recombinase A)
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reca; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  38797 MW;
                                                                                                                                                                                                                                                                                                     69.48;
54.58;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                     Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                           Pred. No. 13;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  A2B70853C26C95FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (class); Thermotogales;
381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no
                                                                                                                                                                                                                                                                                                                                     DB 1; Length 356
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and for
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                           Gaps
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RESULT 7
GGA1_YEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                       STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis B., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Troyaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                      YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                        ear-containing, ARF-binding protein 1). GGA1 OR YDR358W OR D9476.2.
                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGA1 (Golgi-localized, gamma
                                                                                                                                                                                                                                                                                                                     GGA1_YEAST STANDARD;
Q06336;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; pr00297; Ribosomal_L3; 1.
proDom; pD001374; Ribosomal_L3; 1.
proSITE; pS00474; RIBOSOMAL_L3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U13875; AAA21160.2; -. WormPep; C26E6.6; CE26871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative mitochondrial 60S ribosomal protein L3.
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitten (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fulton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000597; Ribosomal_L3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                      164 VRAGIPVKE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VRLGXPVKE 11
               Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42288 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis.

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34;
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3F57FBC8C6F2B667 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 14;
                                                                                                                                                                                                                                                                                                                                                         557 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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TANDER REPORTED DE LA REPORTE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Yeast GGA proteins interact with GTP-bound Arf and facilitate transport through the Goldi."; Yeast 18:1-18(2001).

-1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF MEMBRANE TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00790; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirst J., Lui W.W.Y., Bright N.A., Totty N., Seaman M.N.J., Robinson M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20211637; PubMed=10747088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2] CHARACTERIZATION.
NCBI_TaxID=394;
                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                         Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
                                                                                                                                                                                    Probable trehalose-phosphatase (EC
                                                                                                                                                                                                                                                                                                          P55611;
                                                                                                                                                                                                                                                                                                                                  OTSB_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02883; Alpha_adaptinC2;
Pfam; PF03127; GAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U28372; AAB64793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 GAMMA-ADAPT
-!- SIMILARITY: CONFAINS 1 VHS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21064505; PubMed-11124697; Ehdankina O., Strand N.L., Redmond J.M., Boman A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A family of proteins with gamma-adaptin and VHS domains that
                       Rhizobiaceae; Rhizobium.
                                                                                                                                     OTSB OR Y4PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein transport; Golgi stack; Coiled coil.
DOMAIN 29 165 VHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD003686; HKS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; 1Pk001121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004152; GAT_dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD; S0002766; GGA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: BINDS TO ARF1 AND ARF2
                                                                                                                                                            phosphatase) (TPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002014; HRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 ISVNLGKPIK 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PD021457; Gamma_adaptin_C; SM00288; VHS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                              (Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
ehalose-phosphatase (EC 3.1.3.12) (Trehalose 6-phosphate
                                                                                                                                                                                                                                                                          (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442
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                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DE
Pred. No. 21;
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COILED COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DBA76787E998DBD7 CRC64;
                                                                                                                                                                                                                                                                                                                                  265 AA
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[1] SEQUENCE FROM N.A.

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RESULT 9
YCXB_PORPU
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                             Matches
                                          Query Match
Best Local
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01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 40
Hypothetical 73.8 kD
(ORF621).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     Hypothetical SEQUENCE 67
                                                                                                                                                                                                                                                                                genome."
                                                                                                                                                                                                                                                                                                                       STRAIN=Avonport;
                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.
Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P51234;
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000090; AAB91812.1; -.
InterPro; IPR003337; Trehalose_PPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate.
-!- SIMILARITY: TO THE E.COLI (OTSB) AND YEAST ENZYME (TPS2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 387:394-401(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freiberg C.A., Fellay R.,
                                                                                                                  EMBL; U38804; AAC08120.1; -
                                                                                                                                                                                                                                                                Plant Mol. Biol. Rep. 13:333~335(1995).
                                                                                                                                                                                                                                                                                                         Reith M.E., Munholland J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: Trehalose 6-phosphate + H(2)0 = trehalose
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                             Porphyra purpurea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCXB_PORPU
                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the Porphyra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 LSIRIGPPV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSVRLGXPV 9
   1 LSVRLGXPV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                             Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ar basis of symbiosis between Rhizobium and legumes.";
                                                                                     al protein; Chloroplast.
621 AA; 73754 MW; 36E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid.
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                                Conservative
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34,
40,
kDa
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66.7%;
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                                            67.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
protein in YCF10-PSBI i
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                                          Score 33;
Pred. No.
                              \omega
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                                                                                       36BAF5EBE64F4FBC CRC64;
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                                Mismatches
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37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          intergenic region
                                                                                                                                                                                                                                                                                              purpurea chloroplast
                              سم
••
                                                          Length 621;
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DOMAIN DOMAIN

LDL RECEPTOR BINDING (POTENTIAL).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
8 x 22 AA APPROXIMATE TANDEM REPE

TANDEM REPEATS

DOMAIN

REPEAT REPEAT

REPEAT DOMAIN

REPEAT

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RESULT 10

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                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01442; Apolipoprotein; 1. Glycoprotein; Plasma; Lipid transport; HDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A05312; A05312.
PIR; S33450; S33450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comme entities requires a license agreement (See http://www.isb-sib.ch/annouentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - (- SUBCELLULAR LOCATION: Extracellular.
- (- TISSUE SPECIFICITY: SECRETED IN PLASMA.
- (- SIMILARITY: BELONGS TO THE APOAL / APOAL / APOE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparison of the human, canine and swine E approteins.";
"Comparison of the human, canine and swine E approteins.";
Biochem. Biophys. Res. Commun. 95-374-380(1980).
-I- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimm D.R., Lunney J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98347372; PubMed=9682450; Ramsoondar J.J., Rucker E.B., Vasquez J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brzozowska A.M., Grim
Submitted (MAY-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein E precursor (Apo-E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; x72835; CAA51356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anim. Genet. 29:43-47(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and genetic characterization of the porcine apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                              Heparin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPK000074; Apolipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02649; 10EF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE OF 19-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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| 111 LSIRIGHPI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICKON REMNANT) OF HEPATIC TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U70240;
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7417263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schook L.B.,
                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                        APOLIPOPROTEIN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piedrahita J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                  Chylomicron;
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               вррн8
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                               P57215;
                                       RNFC_BUCAI
                                                   BUCAI
                                                                                                                                                                           Coat protein.
                                                                                                                                                                                                                 or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                          "Nucleotide sequence from bacteriophage phi 80 with high homology the major coat protein gene of lambda."; Nucleic Acids Res. 16:764-764(1988).
-i- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF LAMBDA AND P21.
                                                                                                                                                                                                                                                                                                                                 Kitao S.,
                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage phi-80.
                                                                                                                                                                                                                                                                                                                                                                                                                     Major_head protein (GPE) (GP5) (Major coat protein).
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                                                                                                                                                                                                                                                                                                                                            MEDLINE=88124267;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P05481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                       309 VQLGDPVRE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 LSTRAGQPLRE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSVRLGXPVKE 11
                                                                                                         3 VRLGXPVKE 11
                                                                                                                                                                                     S03314; VHBP80.
                                                                                                                                                                                              X06751; CAA29926.1;
                                                                                                                                                                                                                                                                                                                                 Nakano E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
233
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                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                            PubMed=3267214;
                                                                                                                                                                  38054 MW;
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54.5%;
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V -> L (IN REF. 2).
DE -> EQ (IN REF. 2).
A -> G (IN REF. 2).
Q -> H (IN REF. 2).
Q -> L (IN REF. 2).
N -> I (IN REF. 2).
M -> I (IN REF. 2).
A -> G (IN REF. 2).
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                                                                                                                                      Score 32; DB Pred. No. 32;
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                   BCDAE15ED85785E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                            Mismatches
                                         473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA
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                                                                                                                                              DB 1; Length 341;
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PCL1_ARATH
                                                                                                                                                                            Вþ
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                         Query Match
Best Local :
  SEQUENCE FROM N.A.
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PCL1_ARATH P57681;
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SEQUENCE
                                                         Putative prenylcysteine lyase precursor (EC 4.4.1.18).
AT563910 OR MGI19.4 OR MGI19.11.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
                   Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: Binds 2 4FE-4S clusters (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNFC OR BUll5
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001949; Complex1_51K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001118; BAB12833.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE 4FE4S BACTERIAL-TYPE FERREDOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC
rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: May be part of a membrane complex involved in electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                             272 VRIGTPIK 279
                                                                                                                                                                                                                                                                                                                                                                                                          3 VRLGXPVK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00037; fer4; PF01512; Comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D1512; Complex1_51K; 1.
    PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 AA;
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                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Iron-sulfur; 4Fe-4S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%;
62.5%;
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IRON-SULEUR (4FE-4S)
IRON-SULEUR (4FE-4S)
IRON-SULEUR (4FE-4S)
IRON-SULEUR (4FE-4S)
IRON-SULEUR (4FE-4S)
IRON-SULEUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
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                                          core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 473;
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                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB007646; BAB11039.1; EMBL; AB019227; BAB11039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: INVOLVED IN THE DEGRADATION OF PRENYLATED PROTEINS.
CLEAVES THE THIOSTHER BOND OF PRENYL-L-CYSTEINES, SUCH AS
FRANKESYLCYSTEINE AND GERANYLCFRENVLCYSTEINE (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: A prenyl-L-cysteine + H(2)0 = a prenol + L-
MEDLINE=97045140; PubMed=8890205;
                  SEQUENCE OF 33-330 FROM N.A. STRAIN-ATCC 14028;
                                                                                                                                                     Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                          STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P74884;
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98162728; PubMed=9501997;
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                                                                                  Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEOB_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L5-JUN-2002
L5-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 LTVRLPTPIEE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: FAD (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          iron transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02421; FeoB; TIGRFAMS; TIGR00231;
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                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae.
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PIR; A56932; A56932;
ECOGENE; EGC12102; feoB.
InterPro; IPR003373; FeoB.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR005285; Small_GTP.
Pfam; PF02421; FeoB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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-i- FUNCTION: PROBABLE GTP-DRIVEN TRANSPORTER OF FERROUS ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94012482; PubMed-8407793; Kammler M., Schoen C., Hantke K.; "Characterization of the ferrous iron uptake system of Escherichia coli.";
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TIGRFAMs; TIGR00437; feoB; 1.
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MEDLINE=97426617; PubMed=9278503;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

-L	л л	14 34	13 34	12 34	11 34	10 35	9 36	8 36	7 36	6 36	5 37	4 37	3 38	2 38	1 47	Result No. Score
60	69.4	69.4	69.4	69.4	69.4	71.4	73.5	73.5	73.5	73.5	75.5	75.5	77.6	77.6	95.9	Query Match Length DB
٠ د	301	277	235	124	110	315	753	430	323	277	451	441	324	324	893	ength
9	<u>س</u> 6	5	4	Ν	S	16	17	2	4	4	16	<u>1</u> 6	16	16	16	DB.
084804	Q8RBH7	Q9RTN2	Q8TDV3	Q9RBF8	Q9W4R4	051771	Q9YE62	Q9AF18	P82673	Q9Н044	Q9WY86	OARABO	Q9JSU2	Q9K138	Q9X1V4	ID
+-	Q8rbh7 thermoanaer	Q9rtn2 deinococcus	Q8tdv3 homo sapien	Q9rbf8 alcaligenes	Q9w4r4 drosophila	051771 borrelia bu	Q9ye62 aeropyrum p	Q9af18 agrobacteri	P82673 homo sapien	Q9h044 homo sapien	Q9wy86 thermotoga	Q8ybv0 brucella me·	Q9jsu2 neisseria m	Q9k138 neisseria m	Q9x1v4 thermotoga	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
32	32	32	32	32	32	32	32	32	32	32	32	32	ω w	33	33	33	33	33	33	33	34	34	34	34	34	34	34	34
65.3	ç٦	5	5	S.	65.3	5	Ç.	Š	ū	ū	ū	5	7.	7.	7.	67.3	67.3		67.3		9.	69.4	9	٩.	9	9	69.4	69.4
429	371	37C	363	355	347	311	305	265	249	225	183	99	1490	456	387	386	380	354	324	244	1251	1208	1096	997	985	676	481	362
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Q8UG88	Q8RLH6	Q9M835	Q9RS42	Q9FPH3	Q9YLQ1	Q8YBY5	Q8RL00	Q94BB9	Q9CLS3	Q9x556	Q98RT1	Q71221	P79922	Q918S4	Q9K110	Q45308	Q9UY43	Q92T00	Q8Y0V5	640M8D	Q9PEA2	075162	Q62688	Q15111	Q94JA1	Q97NC0	Q983E2	Q981G4
Q8ug88 agrobacteri	S				Q9ylq1 human immun	Q8yby5 brucella me	77		Q9cls3 pasteurella	~		=	xenopus	xenopus	bacillus			Q92t00 rhizobium m	Q8y0v5 ralstonia s	Q8wqy9 aphrocallis	Q9pea2 xylella fas	075162 homo sapien	rat	-		Q97nc0 streptococc	Q983e2 rhizobium l	Q981g4 rhizobium l

## ALIGNMENTS

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RESULT 2
Q9K138
ID Q9K1
                                                                                                                                                                                RESULT 3
Q9JSU2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
            Q9JSU2;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E. Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00593; pola; 1.
DNA-directed DNA polymerase; Complete proteome.
SEQUENCE 893 AA; 102160 MW; 669EE226DBBB39F3 CRC64;
Hypothetical protein NMA2135.
                                                                                                                                                       Q9JSU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00571; CBS; 2.
Pfam; PF01380; SIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMcd-10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugar isomerase, KpsF/GutQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9K138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMs; TIGR00393; kpsF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                      213 AVRLGTPLKE 222
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                              2 SVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMB0352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE002392; AAF40795.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR004800; KpsF
IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000644; CBS_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. 324 AA; 34155 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                              77.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg J., Jeffries A.C., Nelson K.E., wood D.W., Peden J.F., Dodson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03A3A3BD83B553F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                       324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 893;
                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 4
Q8Y8WO
ID Q8Y8
AC Q8Y8
DT 01-W
DT 01-
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Best Local :
              Matches
                                          Query Match
Best Local
                                                                                                                                                                InterPro; IPR001327; FAD pyr_redox.
Pfam; PF00070; pyr_redox; 1.
Oxidoreductase; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE-20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
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                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00393; kpsF; 1. Hypothetical protein; Complete proteome
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                           Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
                                                                                                                                                                                                                                                                                                                                                                                                               Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae; Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brucella melitensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8YBV0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR004800; KpsF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Z2491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                              EMBL; AE009713; AAL54028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-29459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                               "The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 AVRLGTPLKE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 7; Conserv
                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA;
                                                                                                                                              441 AA;
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                           Kyrpides N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEROGROUP A / SEROTYPE 4A;
                                                                                                                                           Complete proteome
AA; 48477 MW; E91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34144 MW;
                                       75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.6%;
          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:
                                                                       Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB
Pred. No. 9.8;
                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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          Mismatches
                                                                                                                                              E9D846904C6CB5D7 CRC64;
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                                                                       16;
                                                                   Length 441;
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       Indels
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Gaps
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1 LSVRLGXPVKE 11

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RESULT RE
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Query Match
Best Local Similarity
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Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.
                                                                                                                                                                        Submitted (DEC-2000) to the EM EMBL; AL512733; CAC21665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) Hypothetical 32.0 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001949; Complex1_51K.
Pfam; PF01512; Complex1_51K; 1.
Pfam; PF00037; fer4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                          SEQUENCE
                                                                                                                        Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
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01-NOV-1999
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKFZP762P093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9H044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; TM0244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001708; AAD35335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Eyidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TM0244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electron transport complex protein, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9WY86
                                                                                                                                                                                                                                                            TISSUE-MELANOMA;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001450; 4Fe4S_ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 LIVRIGTPVKD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 VEVRLGIPVKD 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LSVRLGXPVKE 11
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                                                                                          277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 AA;
                                                                                                                                                                                                                                 Beyer A., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. 51 AA; 49515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / DSM 3109;
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                                                                                       31950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.5%;
63.6%;
      73.5%;
                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
   Score 36; DE
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7B2D7272CFC6E418 CRC64;
                                                                                          778CCFFC20D1A2E3 CRC64;
                                                                                                                                                                                                                              Weil B., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Kellavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., RR Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Dlake J.A., Brandon R.C., Chiu M.W., Clayton R.A., RA Cline R.T., Colton M.D., Earle-Hughes J., Fine L.D., FitzGerald L.M., Ra FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Ra FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Relley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Kilmek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Ra Klimek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Ra Moreno-Palanques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Ra Moreno-Palanques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Ra Moreno-Palanques R.F., Utterback T.R., Weidman J.F., Li Y., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Colins E.-J., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Ra Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Ra Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Ra Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Ra Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Ra Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Kozak D.L., Ra Bednarik D.P., Cit II., Meissner P.S., Olsen II., Raymond L., Ra Kunsch C., Jill II., Meissner P.S., Clsen II., Raymond L., Ra Venter J.C., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Kannon M.R., Kosen C.A., Haselliue W.A., Fields C., Fraser C.M., Venter J.C.,
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                                                                                                                                                                                                                                                                                                      "Identification of four proteins from the small subunit of the mammalian mitochondrial ribosome using a proteomics approach."; Submitted (JUL-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hilliar L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Hoblifing T., Soares M., "Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLITEL 15, Created)
01-0CT-2000 (TrEMBLITEL 15, Last sequence update)
01-0CT-2000 (TrEMBLITEL 15, Last annotation update)
SEQUENCE
                                                                                                          EMBL; AA314022; -; NOT_ANNOTATED_CDS EMBL; N24248; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                   EMBL; BE242647; -; NOT_ANNOTATED_CDS.
EMBL; AI096645; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 221-323 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Based upon 84 million basepairs of cDNA sequence."; Nature 377:3-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C., rinitial assessment of human gene diversity and expression patterns
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Wei Y., Tsang Y.T.M., Mei G., Ku J.M., Ali-Osman F.R. Jr.,
Bouck J., Gibbs R.A., Margolin J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrial 28S ribosomal protein S28 (MRP-S28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P82673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P82673
                                                                     Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                        Spremulli L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96026280; PubMed=7566098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 183-305 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 8-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
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                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: MITOCHONDRIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Burkhart W., Blackburn K., Moseley A., Koc H.,
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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36844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                POLY-ALA
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B29F819E914F2B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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RESULT 9
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Best Local
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EMBL; AY026066; AAK13016.1; -
EMBL; AY02603662; sub_transporter.
                                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin'no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguch A., Aoki K.-I., Kubota K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                  DNA Res.
                                                                           crenarchaeon,
                                                                                                                              Yamazaki J., Kushida N., Oguchi A., Aoki K.-
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                    STRAIN-KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 18, Last annotation updat.)
7533A long hypothetical aldehyde oxidoreductase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Agrobacterium tumefaciens rnd Homolog Is Required for Trak-
Mediated Quorum-Dependent Activation of Ti Plasmid tra Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21289077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9AF18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9AF18
                                                                                                  "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                     MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APE0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YE62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens.
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InterPro; IPR000674; Aldxan_dh_C
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 LQVRVGVPVEE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 LPVRMGYPVKK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LSVRLGXPVKE 11
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                            AP000060;
                                               naeon, Aeropyrum pernix Kl.";
6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                            BAA79684.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11395455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%;
63.6%;
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63.6%;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313B2FF3D08A1E28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 753 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                     Kosugi H.,
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051771
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Q9W4R4
Query Match

Best Local Similarity

Conhes 6; Conserve
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                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Felschmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fuji C., Cotton M.D., Horst K., Roberts K., Hatch H., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMHITEL 06, Created)
01-JUN-1998 (TREMHITEL 06, Last sequence update)
01-JUN-2002 (TREMHITEL 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              051771
051771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 753 AA;
                                                                  Eukaryota; Metazoa; Arthropoda; Tracheara, Nemera, Muscomorpha; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01315; Ald_xan_dh_C; 1 Pfam; PF02738; Ald_xan_dh_C2;
                                                Ephydroidea: Drosophilidae;
NCBI_TaxID-7227;
                                                                                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                               Q9W4R4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylose operon regulatory protein (XYLR-2)
                                                                                                                                                                                                                   CG13021 protein (AT30881p)
                                                                                                                                                                                                                                                                                                                                                                    Q9W4R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00480; ROK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_Tax1D=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000600; ROK_family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 LAMRLGRPVK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 VAMRLGKPLKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSVRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 вв0831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             АE001181; AAC67180.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   753 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34455 MW; C132BA0030D54B75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.4%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismalches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DE
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6836618422F1322D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                              110 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 315;
                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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SEQUENCE FROM N.A.

Length 124; Indels

0;

Gaps

0;

for Growth

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RESULT 12
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RA Adams D., Celniker S.E., Hit P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Horli J.F., Apdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorson K., Drangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA ROSLEY G. Anvientan A. F. Garra N.S. Gelhart W. M. Classer K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Horstin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit Z.S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
RA Alber M., Zhong F.N., Zhong W., Zhou X., Smith H.O.
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The gen Me sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                         Q9RBF8;
01-MAY-2000
01-MAY-2000
01-JUN-2002
01-MAY-2000 (TREMBLrel. 13, Created)
01-WAY-2000 (TREMBLrel. 13, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Hypothetical 13.7 kDa protein (Fragment).
Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003427; AAF45879.1; -.
EMBL; AY075295; AAF468163.1; -.
ENBL; AY075295; AAF68163.1; -.
ENBL; AY075295; CG13021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kromiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                       Q9RBF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker S.
                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSVRLGXPVK
                                                                                                                                                                                                                                                                                                                                                              INVRIGNPIK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brokstein P., Hong L., Agbayani A., avez C., Dorsett V., Dresnek D., Far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11901 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B61518F244C49545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carlson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ketchum K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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ID 870V3
ID 2010V3
AC Q8
DT 001
DT 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                      Q9RTN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                      Q9RTN2;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Takeda S., Kadowaki S
"Identification of G
genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TDV3;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF130250; AAD55889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seibert V., Schloemann M.;
"Characterization of a Gene Cluster Encoding the Maleylacetate
Reductase from Raistonia eutropha 335, an Enzyme Recruited for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia.
NCBI_TaxID=510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TDV3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with 4-Fluorobenzoate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                  Hypothetical DR1728.
                                                                                                                                                                                                                                                                                                                                                              Q9RTN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL; AB083587; BAB89300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
         SEQUENCE FROM N.A
                                                                                            Deinococcaceae;
                                                                                                                    Bacteria;
                                                                                                                                                      Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VRLGNPFKE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSVRLGXP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
7; Conser
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                                                                                     Thermus/Deinococcus aceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA;
                                                                                                                                                                                                                                      O (TrEMBLrel. 13, CTREMBLrel. 13, CTREMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                          protein DR1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Buteleostomi;
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87.5%;
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protein-coupled
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77.8%;
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21, Last sequence update)
21, Last annotation update)
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                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                       group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98107180D7D6B308 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3DE99E10EF97EB8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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pled receptor genes
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Best Local Similarity
Thehes 7; Conserva
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Search completed: January 15, 2003, 12:35:56
Job time: 33.5714 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter tengcongensis.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
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Pfam; PF03618; DUF299; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 277 AA; 30170 MW; FB133B5339C6BF2B CRC64;
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-21992816; PubMed-11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane proteins related to metalloendopeptidases. NLPD2 OR TTE0841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Science 286.1571-1577(1999).
EMBL; AE002014; AAF11284.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8RBH7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
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                                                                                                                                                   205 ISVHIGTPVK 214
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                                                                                                                                                                                                                     1 LSVRLGXPVK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AA; 33068 MW; 080B887435B3197B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 34; DB 16; Length 277; 63.6%; Pred. No. 58; ative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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-MODEL-frame+_p2n.model -DEV-xlh
-Q=/cgn2_1/USPTO_spool/US09823649/runat_14012003_151002_29139/app_query.fasta_1.1393
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTEMT=pto -NORH=ext -HEAPSIZE=-500 -MINLEN=0 -MAXLEN=200000000
-USER=US09823649_eCGN_1_1378__grunat_14012003_151002_29139 -NCU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARM_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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49
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 GenEmbl:*
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Listing first 45 summaries
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gb_ph:*
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gb_un:*
gb_vi:*
em_ba:*
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em_pat:*
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RESULT 1
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_ariv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pas:*
35: em_htg_pas:*
36: em_htg_rod:*
37: em_htg_rod:*
38: em_y:*
40: em_htgo_nus:*
41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 38 from patent US 6077664.
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Slater, M.R., Huang, F., Hartnett, J.R., Bolchakova, E., Storts, D.R., Otto, P., Miller, K.M., Novikov, A. and Velikodvorskaya, G.A.
Thermophilic DNA polymerases from Thermotoga neapolitana Patent: US 6077664-A 36 20-JUN-2000;
1 (bases 1 to 1737)
Slater, M.R., Huang, F., Hartnett, J.R., Bolchakova, E., Storts, D.R., Otto, P., Miller, K.M., Novikov, A. and Velikodvorskaya, G.A. Thermophilic DNA polymerases from Thermotoga ncapolitana
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                                                 1 (bases 1 to 1833)
Slator, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 15 14-DEC-1999;
                                                                                                                                                                         Sequence 15 from patent US 6001645. AR094377
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Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 18 14 DEC-1999;
Location/Qualifiers
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Thermophilic DNA polymerases from thermotoga neapolitana
Patent: US 6001645-A 28 14-DEC-1999;
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Slatcr,M.R., Huang,F. and Hartnett,J.R.
Thermophilic DNA polymerases from thermotoga neapolitana
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Slater, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymersses from thermotoga neapolitana
Patent: US 6001645-A 34 14-DEC-1999;
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Slater, M.R., Huang, F. and Hartnett, J.R.
Thermophilic DNA polymerases from thermotoga meapolitana patent: US 6001645-A 32 14-DEC-1999;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
AARJON 2
AATJON AATJO

Thermotoga neapolitana strain DSM 5068.

/\*tag= a

Location/Qualifiers

thermostable enzyme; ss.

DNA polymerase; Tne; DNA sequencing; amplification;

The DNA polymerase C-terminal region DNA.

15-AUG-1996 (first entry)

AAT30049;

AAT30049 standard; DNA; 694 BP.

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA fragment (AAT30049) codes for the C-terminal portion (AAR9814) of the 100 kba thermostable DNA polymerase (AAR98143) of Thermotogs neapolitana (Tne), including the O helical region. Tha polymerase is a thermostable enzyme suitable for use in DNA sequencing and amplification reactions. It can be obtd. by obtd. from transformed host cells, e.g. E. coli, carrying the DNA polymerase gene. Mutants having improved enzymatic properties may be produced (see also AAR98144-47).
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       08-SEP 1995;
                                               14-AUG-1996;
                                                                                                                  06-SEP-1996;
                                                                                                                                                                                             13-MAR-1997
                                                                                                                                                                                                                                                                                                                                   Thermotoga neapolitana strain DSM 5068
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase; Tne; exonuclease; DNA amplification; DNA sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga neapolitana DNA polymerase C-terminal region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Fig 5A-B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga neopolitana DNA polymerase and thermostable mutants useful in DNA sequencing and amplification reactions  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR98144.
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30-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                              enzyme engineering; protein engineering; mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT60031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT60031 standard; DNA; 694 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-209362/21.
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94US-0316423.
       95US-0525057
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/transl_except= (671..673, aa:Ser)
/transl_except= (674..676, aa:Ile)
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02-OCT-1995;
21-DEC-1995;
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                                       06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T. neapolitana Tne polymerase C-terminal cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 694 BP; 230 A; 136 C; 178 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase is given in AAT60032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chatterjee DK,
                                                                                                                  18-JAN-2000
                                                                                                                                                                                         US6015668-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotoga neapolitana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase; Poll; O-helix; DNA sequencing; amplification; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for DNA amplification, synthesis and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 CTTTCTCTCAGACTTGGAATACCGGTTAAAGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUGHES A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0537397.
95US-0537400.
95US-0576759.
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                                       9608-0706706
                                                                                                                                                                                                                                                        /product= "Tne"
/note= "partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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Miller KM,

Otto P;

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US-09-823-649A-5 (1-11) x AAZ88767 (1-694)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-1995;
08-SEP-1995;
02-OCT-1995;
21-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence more than 500 bases; reduce false stops in the sequence ladder; reduce template requirements 10-fold (when using 355 labeling); and also requirements for primer and labeled terminator. They increase sequencing efficiency with structure-containing or GC-rich templates; reduce film
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   templates. (I) have higher thermostability than known enzymes (e.g. 50% retention of activity after 60 min at 90 pusso), and may be free of exonuclease activity and/or ability to discriminate against dideoxynucleotides (ddNTP). They permit sequencing at high temperature provide strong, clear sequences (increased signal-to-noise ratio); can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exposure times; do not generate sequencing artefacts with homopolymeric sequences and allow quantitation of bases in heterologous mixtures. This sequence encodes the Thermotoga neapolitana The polymerase carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel methods for sequencing DNA, amplifying double-stranded DNA or synthesizing DNA which use a mutant Thermotoga neapolitana DNA polymerase (I) or its fragments. (I) are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Thermotoga neapolitana polymerase with reduced exonuclease activity or reduced discrimination against dideoxynucleotides
      WO9641014-A1
                                          Synthetic.
                                                                              polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                 DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                               Thermotoga neapolitana DNA polymerase Tne M284 delB gene.
                                                                                                                                                                                                                                              AAT58155;
                                                                                                                                                                                                                                                                                    AAT58155 standard; DNA; 1485 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 694 BP; 229 A; 136 C; 179 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods, also for DNA labeling and for synthesis of cDNA from templates. (I) have higher thermostability than known enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing, amplification and synthesis of DNA by essentially standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Column 51-54; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequencing, amplification and synthesis methods, using mutant forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hughes AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1995;
30-SEP-1994;
                                                                                                                                                                                                        15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal which is described in the method of the invertion.
                                                                                                                                                                                                                                                                                                                                                                   233 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                           1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-181138/16.
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                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0525057.
95US-0537400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0576759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0370190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0537397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT58145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-823-649A-5 (1-11) x AAT58155 (1-1485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and also has amino acid residues 309-424 of the 3' exonuclease domain deleted. The DNA construct was obtd. by restriction digestion of pM284-derived DNA (see also AAT58135). When expressed in E. coli, The M284 delB showed no detectable polymerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA sequence (AAV58155) encodes deletion mutant The M284 delB (AAW11525) of the DNA polymerase (see also AAW11513) of Thermott neapolitana. The deletion mutant lacks the N-terminal 283 amino acids from the 5' exonuclease domain of the native enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024 CTTTCTCTGAGACTTGGAATACCGGTTAAAGAA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 174-175; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable DNA polymerase from Thermotoga neapolitana – useful in DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052374/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolchakova E,
                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                              DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                            Thermotoga neapolitana DNA polymerase Tne M323 gene
                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT58145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1485 BP; 490 A; 312 C; 365 G; 318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW11525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996
  (PROM-) PROMEGA CORP.
                                          07-JUN-1995;
                                                           31-MAY-1996;
                                                                                                    07-JUN-1996;
                                                                                                                                                                                  W09641014-A1
                                                                                                                                                                                                                                                             polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT58145 standard; DNA; 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In contrast, a Tne M284 mutant (see also AAW11514) was active.
                                                                                                                                          19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuSerValArqLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0484661
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                                        96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0656664
                                                                                                    96WO-US09641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA sequence (AAT58145) encodes deletion mutant The M323 (AAW11524) of the DNA polymerase (see also AAW11513) of Thermotoga neapolitana. The M323 has an artificially created methionine at amino acid position 323 as the initiator methionine in the 3' exonuclease domain of the enzyme. When expressed in E. coli, The M323 showed
                                                                                                                                                                                                                                                                                                                                                                                                        1255 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1287
Example 3; Page 133-135; 200pp; English.
                  Thermostable DNA polymerase from Thermotoga neapolitana - useful in DNA sequencing or for amplification of double stranded DNA
                                                    P-PSDB; AAW11523
                                                                                  Slater MR,
                                                                                            Bolchakova E,
                                                                                                                                     31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                    07-JUN-1996;
                                                                                                                                                                                                               WO9641014-Al.
                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                           DNA polymerase; The;
                                                                                                                                                                                                                                                                                                 Thermotoga neapolitana DNA polymerase Tne M316 gene.
                                                                                                                                                                                                                                                                                                                      15-APR-1997
                                                                                                                                                                                                                                                                                                                                           AAT58144;
                                                                                                                                                                                                                                                                                                                                                                AAT58144 standard; DNA; 1737 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1719 BP; 553 A; 367 C; 413 G; 386 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no detectable polymerase activity. In contrast, a Tne M284 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 169-172; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW11524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolchakova E,
                                                                                                                 (PROM-) PROMEGA CORP.
                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                       polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss.
                                                                                                                                                                                                                                                                  thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (see also AAW11514) was active.
                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                              1997-052374/05.
                                                                                 Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Storts DR;
                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                            Hartnett JR,
                                                                                                                                    96US-0656664
95US-0484661
                                                                                                                                                                    96WO-US09641
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95.92%
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                                                                                                                                                                                                                                                                          thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang F,
                                                                                            Huang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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                                                                                              Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Otto P;
                                                                                              Otto P;
                                                                                                                                                                                                                       CCCCCCCX PX PHX DR
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US-09-823-649A-5 (1-11) x AAT58144 (1-1737)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the DNA polymerase (see also AAWI1513) of Thermotoga neapolitana. The M316 has an artificially created methion and at mino acid position 316 as the initiator methionine. It was created by introducing a Met residue at position 316 (and a corresponding NCOI site) via site-directed mutagenesis of the native The gene (see also AATS8134). When expressed in E. coli from a T7 or tro
                       A DNA sequence (AAT58135) in plasmid pM284 codes for modified DNA polymerase The M284 (AAW11514) in which amino acids 1-283 of the native Thermotoga neapoiltana enzyme (see also AAW11513) are deleted and the naturally occurring Met-284 residue becomes the initiating methionine. It was obtd. by restriction digestion of the native gene (AAT58134). The deleteion results in elimination of 5' exonuclease activity. Further modification of the DNA in pM284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1276 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase: Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT58135 standard; DNA; 1833 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA sequence (AAT58144) encodes deletion mutant The M316 (AAW11523)
                                                                                                                                                                                                                                                                                   Claim 20; Page 128-131; 200pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga neapolitana DNA polymerase Tne M284 gene
exonuclease activity. Further modification of the DNA in pM284 (see also AAT58136-43) yield mutant enzymes (AAW11515-22) that also
                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW11514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l LeuSerValArgLeuGly***ProValLySGlu 11
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950S-0484661
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                                               A DNA sequence (AAT58136) codes for mutant thermostable DNA polymerase The M284(D323E) (AAW1515) in which amino acids 1.283 of the native Thermotoga neapolitana enzyme (see also AAM15813) are deleted and amino acid residue 323 (Asp) of native The is substd. by Glu. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of The M284(D323E) in transformed host cells. The mutant enzyme has no significant 5' or 3' exonuclease activity and
e.g. PCR.
                                                                                                                                                                                                                                                                                          Claim 20; Page 138-140; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1996;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplifications, esp. PCR.
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are useful in DNA sequencing reactions and nucleic acid
                              is suitable for use in DNA sequencing and amplification reactions,
                                                                                                                                                                                                                                                                                                                                               DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW11515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga neapolitana DNA polymerase Tne M284(D323E) gene
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                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROM-) PROMEGA CORP.
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                              A DNA sequence (AAT58137) codes for mutant thermostable DNA polymerase The M284(B325D) (AAWI1516) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAWI1513) are deleted and amino acid residue 325 (Glu) of native Tne is substd. by Asp. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAV58135). The mutated gene can be incorporated into a vector and used for prodn. of Tne M284(B325D) in transformed host cells. The mutant enzyme has no significant 5' or 3' exonuclease activity and is sultable for use in DNA sequencing and amplification reactions,
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No.:
                        e.g. PCR
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                                                                                                                                                                                   Claim 20; Page 142-144; 200pp; English.
                                                                                                                                                                                                             DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                            Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                           P-PSDB; AAW11516,
                                                                                                                                                                                                                                                                          WPI; 1997-052374/05
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Sequence 1833 BP; 590 A; 395 C; 440 G; 408 T; 0 other,

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-823-649A-5 (1-11) x AAT58137 (1-1833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                     used for prodn. of The M284(Y464F) in transformed host cells. mutant enzyme has no significant 5' exonuclease activity and reduced 3' exonuclease activity. It is suitable for use in DNA
                                                                                                                                                                                                                                                                     A DNA sequence (AAT58138) codes for mutant thermostable DNA polymerase The M284(Y464F) (AAW11517) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 464 (Tyr) of native The is substd. by Phe. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and
                                                                                                          Sequence 1833 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 147-149; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT58138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                sequencing and amplification reactions, e.g. PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-052374/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9641014-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; Tne; thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga neapolitana DNA polymerase Tne M284(Y464F) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT58138 standard; DNA; 1833 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW11517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag---a*
/note= "base 542 (T) is A in the native Tne gene"
                                                                                                          590 A; 393 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.91%
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47.00
                             1.49
  47.00
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                                                                                                          440 G; 410 T;
  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
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                                                                                                       0 other;
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Query Match:

Best Local Similarity: Percent Similarity:

47.00 90.91% 90.91% 95.92% 1.49

Mismatches:

1833 10 0 1

Matches:

Indels: Conservative: Pred. No.: Alignment Scores:

Sequence 1833 BP; 591 A; 394 C; 439 G; 409 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                         mutant enzyme has no significant 5' exonuclease activity and reduced 3' exonuclease activity. It is suitable for use in DNA
                                                                                   Thermologa neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 468 (Asp) of native Tne is substd. by Asn. It was obtd. by site-directed mutagenesis of pM284 DNA (see also
                                                                                                                             A DNA sequence (AAUS8139) codes for mutant thermostable DNA polymerase The M284(Y464F) (AAW11518) in which amino acids 1-283 of the native
           sequencing and amplification reactions, e.g. PCR.
                                                                                                                                                                         Claim 20; Page 151-154; 200pp; English.
                                                                                                                                                                                                      DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                               Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09641014-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermotoga neapolitana DNA polymerase Tne M284(D468N) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT58139 standard; DNA; 1833 BP
                                                        used for prodn.
                                                                         AAT58135).
                                                                                                                                                                                                                  Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                            Bolchakova E,
                                                                                                                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT58139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LeuSerValArgieuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                1997-052374/05.
                                                                                                                                                                                                                                                     AAWII'S B.
                                                                                                                                                                                                                                                                                              Storts DR
                                                     The mutated gene can be incorporated into a vector and of The M284 (D468N) in transformed host cells. The
                                                                                                                                                                                                                                                                                                            Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                                        96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US09641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "base 553 (A) is G in the mative The gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.91%
90.91%
95.92%
                                                                                                                                                                                                                                                                                                            Huang F, Miller KM,
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                            Otto P;
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US-09-823-649A-5 (1-11) x AAT58139 (1-1833)
                                                          Query Match:
                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                            Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                     A DNA sequence (AAT58140) codes for mutant thermostable DNA polymerase The M284(D3218) (AAW11519) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW1513) are deleted and amino acid residue 323 (Asp) of native Tne is substd. by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAM50315)
                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slater MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1006;
07-JUN-19.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga ncapolitana; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga
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                                                                                                                                                                                                     Sequence 1833 BP; 590 A; 395
                                                                                                                                                                                                                                            amplification reactions, e.g. PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT58140 standard; DNA; 1833 BP
                                                                                                                                                                                                                                                                   mutant enzyme is suitable for use in DNA sequencing and
                                                                                                                                                                                                                                                                                     AAT58135). The mutated gene can be incorporated into a vector used for prodn. of The M284(D323A) in transformed host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW11519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-052374/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Page 156-158; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neapolitana DNA polymerase Tne M284(D323A) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0656664.
95US-0484661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hartnett JR,
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                                      1.49
47.00
90.91%
90.91%
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18
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                                                                                                                                                                                                     C; 440 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang
                                                                                                   Conservative:
                                                            Indels:
                                                                                Mismatches:
                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n,
                                                                                                                                                                                                         408
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ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A in the native Tne gene"
                                                                                                                                                                                                         Τ;
                                                                                                                                                                                                         0 other;
                                                                                                   1333
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                                                                                                                                                                                                                                                                 ARTSULT 13
ART58141
ID ART58
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               8
                                                        US-09-823-649A-5 (1-11) x AAT58141 (1-1833)
                                                                                                     DB:
                                                                                                                                                                                 Score:
                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                       Query Match:
                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                               The M284(D323E) (AAW11520) in which amino acids 1-283 of the native "hermotoga neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 389 (Asp) of native The is substd. by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of The M284(D389A) in transformed host cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                                                                                                                                                          mutant enzyme is suitable for use in DNA sequencing and amplification reactions, e.g. PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 161-163; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostable DNA polymerase from Thermotoga neapolitana - \mbox{\scriptsize DNA} sequencing or for amplification of double stranded DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1996;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermotoga neapolitana DNA polymerase Tne M284(D389A)
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                                                                                                                                                                                                                                                                 Sequence 1833 BP; 590 A;
                                                                                                                                                                                                                                                                                                        amplification reactions, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA sequence (AAT58141) codes for mutant thermostable DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW11520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bolchakova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996
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LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                          Similarity:
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95US-0484661
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/*tag=_a
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                                                                                                                                                                                                                                                                 C; 441 G; 408 T; 0 other;
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US-09-823-649A-5 (1-11) x AAT58140 (1-1833)

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1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404

1833 10 0 1 0

Page 7

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Query Match:
                                                                                         Alignment Scores: Pred. No.:
US-09-823-649A-5 (1-11) x AAT58142 (1-1833)
                                                   Best Local Similarity:
                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                   A DNA sequence (AAT58142) codes for mutant thermostable DNA polymerase Tne MS84(D323E,D389A) (AAW1521) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW1513) are deleted and amino acid residue 323 (Asp) of native Tne is substd. by Ala, and Asp-389 by Ala. It was obtd. by site-directed mutagenesis of pM284 DNA (see also AAT58135). The mutated gene can be incorporated into a vector and used for prodn. of the triple mutant in transformed host cells. The triple mutant has no significant 5' or 3' exonuclease activity and a half-life at 97.5 deg C of 22 min compared with 5 min for native Tne and 8 min for native Taq. It is suitable for use in DNA sequencing and amplification reactions,
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; Tne; thermostable enzyme; protein engineering; thermosta: lity; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana; ss.
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                                                                                                                                Sequence 1833
                                                                                                                                                                                                                                                                                                                                Claim 20; Page 165-167; 200pp; English.
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95US-0484661
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317..318
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                                                                                                                                441 G; 408
                                  Conservative: Mismatches: Indels:
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              Percent Similarity:
                                              Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  made in the 3' exonuclease domain of the enzyme. It was obtd. I site-directed mutagenesis of DNA (AATS8142) coding for a triple mutant. The mutated gene can be incorporated into a vector and used for prodn. of The Quad in transformed host cells for use IDNA amplification reactions and esp. for radioactive sequence
                                                                                                                                                   A DNA sequence (AAT58143) codes for mutant thermostable DNA polymerase The Quad (AAW11522) in which amino acids 1-283 of the native Thermotoga neapolitana enzyme (see also AAW11513) are deleted and amino acid residue 3 amino acid substims. (D323A, D389A, F730Y) are made in the 3' exonuclease domain of the enzyme. It was obtd. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase; "Inc; Quad polymerase; thermostable enzyme; protein engineering; thermostability; DNA sequencing; PCR; polymerase chain reaction; amplification; exonuclease;
                                                                                                                                                                                                                           Claim 20; Page 180-182; 200pp; English.
                                                                                                                                                                                                                                                 Thermostable DNA polymerase from Thermotoga neapolitana - useful in DNA sequencing or for amplification of double stranded DNA
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07-JUN-1995;
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                                                                        Sequence 1833
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317..318
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Best Local Similarity:

Mismatches:

Search completed: January 15, 2003, 12:55:39 Job time : 137.143 secs US-09-823-649A-5 (1-11) x AAT58143 (1-1833) Query Match: DB: 95.92**%** 18 Indels:
Gaps: 00

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7, Appli 18, Appl 22, Appl 22, Appl 32, Appl 32, Appl 34, Appl 15, Appl 26, Appl 27, Appl 28, Appl 28, Appl 28, Appl 29, Appl 21, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 21, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 20, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 28, Appl 29, Appl 20, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 28, Appl 28, Appl 29, Appl 20, Appl 21, Appl 21, Appl 22, Appl 23, Appl 24, Appl 25, Appl 26, Appl 27, Appl 28, Appl 28,

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is derived by analysis of the total score distribution.
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Ygapop 10.0 , X
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
        REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 30-SEP-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 01 APPLICATION NUMBER: U
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                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                           NAME: Esmond, Robert REGISTRATION NUMBER:
                                                                                                                                           FILING DATE: 09-JAN-1995
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-656-664-25
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US-07-971-819A-1
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US-08-458-819-3
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US-09-823-649A-5 (1-11) x US-08-537-400-15 (1-694)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chatterjee, D6b K.
TITLE OF INVENTION: Cloned DNA Polymerases from
TITLE OF INVENTION: maritima and Mutants Thereof
                                                                                                                                               APPLICATION NUMBER: US 08/537,397 FILING DATE: 02-OCT-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                            ATTORNEY/AGENT INFORMATION:
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               TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                    NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 08-SEP-1995
                                                                                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                     REFERENCE/DOCKET NUMBER: 0942.2800006
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NVENTION: Cloned DNA Polymerases from Thermotoga
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APPLICATION NUMBER: US 08
FILING DATE: 01-JAN-1995
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,397
FILING DATH: 02-OCT-1995
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: US 08/537,400
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COMPUTER: LBM ITO OPERATING SYSTEM:

SYSTEM: PC DOS/MS-DOS

SOFTWARE:

Patentin Release #1.0, Version #1.30

FILING DATE:

02-OCT-1995

US 08/370,190

FILING DATE:

14-AUG-1996

US 08/689,807

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

06-SEP-1996

US/08/706,706

APPLICATION NUMBER:

08-SEP-1995

US 08/525,057

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Query Match:
                                                                                                                                                                                                                                      US-08-706-706-17
                                                                                                                                                                                                                                                                                                                                           US-09-823-649A-5 (1-11) x US-08-706-702-17 (1-694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                    patent No. 6015668
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                    APPLICANT: Chatterjee, Deb K.
APPLICANT: Chatterjee, Deb K.

""" OF INVENTION: Cloned DNA Polymerases from Thermotoga and
                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                 233 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                      STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MEDIUM TYPE:
                                           COUNTRY:
                                                           STATE:
                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                 1 LeuSerValArgLeuGly***ProValLysGlu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                               20005-3934
                                                            Z
                                                                                    E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 New York Ave., N.W., Suite 600
                                             OSA
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2..691
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Floppy disk
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90.918
95.928
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47.00
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Matches:
Conservative:
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US-09-823-649A-5 (1-11) x US-08-706-706-17 (1-694)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-484-661A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1485 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6001645
GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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LOCATION:
                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/484,661A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                           NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRMG-01175
                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
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STRANDEDNESS:
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double
                   acid
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                               Alignment Scores:
                                                              US-08-656-664-38
                  Pred. No.:
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                                                                                                                                                                                                                      TELEFAX: (415) 397-833 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1024 CTTTCTGTGAGACTTTGGAATACCGGTTAAAGAA 1056
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                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRING Application Data:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 240 CITY: San Francisco
CITY: San Francisco
STATE: California
****i+ed Stat/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Otto, Paul
TITLE OF INVENTION: THERMOPHILIC DNA POLYMI
TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                          FEATURE:
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LOCATION:
                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM MC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                         TOPOLOGY:
                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                          TYPE:
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                                                                                                                                                                                                                                                                                                                    NAME:
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                                                                                                                                                                                       LENGTH:
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6077664
                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                             Ingolia, Diane E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 Montgomery Street, Suite 2200
                                                                                                                                                                                    1485 base pairs
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                                                                                                                                                                                                                                     (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolchakova, Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang, Fen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slater, Michael R.
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                                                                                          CDS
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                                                                           1.,1482
                                                                                                                                                                                                                                                      (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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N: 435
                                                                                                                                                        double
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Length:
Matches:
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Score:

Conservative:

RESULT 7

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Best Local Similarity:
                                                         US-09-823-649A-5 (1-11) x PCT-US96-09641-38 (1-1485)
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                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                       Query Match:
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                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  . No.:
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1485 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1024 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1056
1024 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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COMPUTER: IB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
              1 LeuSerValArgLeuGly***ProValLysGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Medlen & Carroll
220 Montgomery Street, Suite 2200
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Storts, Douglas R.
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                                                                                                                                                                                                                                                                                                                                                                                       (415) 705-8410
415) 397-8338
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                    Patent No.
                                                                                                                                                    Sequence 36,
                                                                                                GENERAL INFORMATION:
APPLICANT: Slater
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TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                       1255 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1287
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LENGTH: 1716 base pairs
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM
                                  APPLICANT:
                                                                  APPLICANT:
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                   APPLICANT:
                                                   APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lir
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                                                                                                                                    6, Application US/08656664
6077664
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Huang, Fen
                            Bolchakova, Elena
Storts, Douglas R.
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                 Otto,
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                                                                Hartnett, James R.
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Conservative:
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PCT-US96-09641-36; Sequence 36, Application PC/TUS9609641
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STATE: California
Onited Stat
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   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                      TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 57
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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NUMBER OF SEQUENCES:
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                                                    COUNTRY:
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                                                                                     SSEE: Medlen & Carroll
T: 220 Montgomery Street,
San Francisco
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ATION NUMBER: 40,027
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United States Of America
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Floppy disk
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                                                                                                       Suite 2200
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                   COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: MEDIEN & CARROLL
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LENGTH: 1716 base pairs
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REFERENCE/DOCKET NUMBER: PR
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HOLCHAROVA, ELENA
TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HUANG, FEN APPLICANT: BOLCHAKOVA,
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                                                                                  APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO
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                                NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027
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                                                                                       07-JUN-1995
N: 435
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                  PRMG-01175
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                                                                                                                                                       Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10,
                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 APPLICATION NUMBER: US/08/656
FILING DATE: 31-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1276 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1308
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LENGTH: 1737 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll
STREET: 220 Wontgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FEATURE:
            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Otto, Paul
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                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lin
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Huang, Fen
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Percent Similarity:
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    Query Match:
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                            Percent Similarity:
Best Local Similarity:
               Query Match:
                                                                                       Alignment Scores:
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                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application PC/TUS9609641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1276 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                     NAME/KEY .
LOCATION:
                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: PR
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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Storts, Douglas R.
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Conservative:
              Mismatches:
Indels:
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                                           Conservative:
                                                          Matches:
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APPLICANT:

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US-08-484-661A-15; Sequence 15, Application US/08484661A; Patent No. 6001645
                                                                       RESULT 14
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                                                                                                                                                                                    US-09-823-649A-5 (1-11) x US-08-484-661A-7 (1-1833)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6001645
GENERAL INFORMATION:
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                                                                                                           1372 CTTTCTGTGAGACTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOLCHAKOVA, ELENA
TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: PROM THERMOTOGA NEAPOLITANA
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                        NO . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
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                                                                                                                                               1 LeuSerValArgLeuGly***ProValLysGlu 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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Matches:
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US-09-823-649A-5 (1-11) x US-08-484-661A-15 (1-1833)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                        US-08-484-661A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                              ; Patent No. 6001645
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                  Sequence 18, Application US/08484661A
                                                                                                                                                                                                                                                                                                                                                1372 CTTTCTGTGAGACTTTGGAATACCGGTTAAAGAA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTHM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
AFTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANI: BOLCHAKOVA, ELENA
TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                            TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 51
                                                                                                                                                                                        APPLICANT: SLATER, MICHAEL R. APPLICANT: HARTNETT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/484,661A FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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STATE: CALIFORNIA
                                      STREET:
                                                      ADDRESSEE:
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                    SAN FRANCISCO
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220 MONTGOMERY STREET,
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                                                                                                                                                  HUANG, FEN
BOLCHAKOVA, ELENA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/484,661A
FILING DATE: 07-7UN-1995
CLASSIFICATION *1.435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRMG-01175
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1833 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
Search completed: January 15, 2003, 12:58:49 Job time : 29 secs
                                                                                                                                                               Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 1..1830
US-08-484-661A-18
                                                                                                                                US-09-823-649A-5 (1-11) x US-08-484-661A-18 (1-1833)
                                                                                                                                                                                                                                                 Alignment Scores: Pred. No.:
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                                                              COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
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47.-00
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Minimum DB seq
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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protein search, using sw model
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49
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PIR_73:*
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Listing first 45 summaries
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pir3:*,
pir4:*
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E72398
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S73155
JC5145
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C82721
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G81207
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A; Molecule type: DNA A; Residues: 1-893 <ARN>

A; Cross-references: GB: AE001805;

GB:AE000512; NID:g4982180; PIDN:AAD36686.1; PID:g498

A; Status: preliminary

Nature 399, 323-329, 1999

A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A, Reference number: A72200; MUID:99287316; PMID:10360571
A, Accession: E72232

## ALIGNMENTS

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000
C;Accession: E72332

DNA-directed DNA polymerase I - Thermotoga maritima (strain MSB8)

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

RESULT 1 E72232

RESULT 2 D81785 A;Molecule type: DNA A;Residues: 1-324 <PAR> A;Residues: 1-324 <PAR> A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85347.1; PID:g738 A;Experimental source: serogroup A, strain Z2491 C;Genetics: C.Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001 C;Accession: D81785
C;Accession: D81785
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81785 C:Genetics:
A:Gene: TM1619
C:Superfamily: DNA-directed DNA polymerase I A;Gene: NMA2135 C;Superfamily: probable ATP-binding protein gutQ; CBS homology Ω C; Species: Neisseria meningitidis conserved hypothetical protein NMA2135 [imported] - Neisseria meningitidis (strain da A; Experimental source: strain MSB8 A;Status: Query Match
Best Local Similarity
Matches 10; Conserv 741 LSVRLGVPVKE 751 1 LSVRLGXPVKE 11 preliminary Conservative 90.9%; 95.9%; 0; Score 47; DB 2 Pred. No. 0.17; Mismatches DB 2; Length 893; Indels 0 Gaps 0; 22

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81207
                                                                                                                                                                                     A; Map position: II
C; Superfamily: NADH dehydrogenase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-324 <TET>
A;Residues: 1-324 <TET>
A;Cross-references: GB:AE002392; GB:AE002098; NID:g7225573; PIDN:AAF40795.1; PID:g722557
A:Experimental source: serogroup B, strain MC58
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                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
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C; Superfamily:
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A; Residues: 1-441 < KUR>
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A;Accession: AI3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                           A; Gene: BMEII0786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: AI3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADH2 dehydrogenase (EC 1.6.99.3) [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                    247 VEVRLGIPVKD 257
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                                                              1 LSVRLGXPVKE 11
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Pred. No.
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Pred. No.
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Pred. No.
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Dougherty, B.A.
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                                            Matches
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Best Local
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                                                              Local
1 LSVRLGXPVKE 11
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A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914 R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P. Biochemistry 20, 7010-7015, 1981
A;Pitle: Rat angiotensinogen and Des(antiotensinI)angiotensinogen: purification, cha; A;Reference number: A90456; MUID:82091819; PMID:6797467
A;Accession: A90456
                                                                                                                                                                                                                                                                                                                                                                  A; Noiecule type: protein
A; Residues: 25-41 <BOU>
C; Comment: Anglotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C; Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Contains: angiotensin I; angiotensin II; angiotensin III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 **sequence_revision 13-Jun-1983 **text_change 18-Jun-1999
C;Accession: A93945; A90456; A01251
R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.
A;Reference number: A93945; MUID:83169849; pMID:6572971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: E72398
C;Accession: E72398
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
                                                                                                                       F;25-34/Product: angiotensin I *status experimental <PP1>
F;25-32/Product: angiotensin II *status experimental <PP2>
F;26-32/Product: angiotensin III *status experimental <PP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein TM0244 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                       F;1-24/Domain: signal sequence #status predicted <SIG>F;25-477/Product: angiotensinogen #status predicted <MPT>
                                                                                                                                                                                                                                                                            C: Keywords: blood pressure control; glycoprotein; liver; plasma;
                                                                                                                                                                                                                                                                                                                          C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-477 < OHK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A93945
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                                                                                         F;295,319/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiotensin precursor - rat
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A;Experimental source: strain MSB8
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Best Local
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Similarity 63.6%;
7; Conservation
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73.5%;
72.7%;
Score 36;
Pred. No.
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Pred. No.
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DB 1;
17;
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Similarity 8; Conserv Conservative

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Mismatches

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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                               C;Accession: E75361
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
                                                                                                                conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable aldehyde oxidoreductase APE0708 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xylose operon regulatory protein (xylR-2) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: F70203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001181; GB:AE000783; NID:g2688772; A;Experimental source: strain B31 C;Superiamily: glucose kinase; glucose kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID: 98065943; PMID: 9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: carbon-monoxide dehydrogenase large chain
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A; Residues: 1-753 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi,
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ya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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70.0%;
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattorı, M.; Sni
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99927
                             A; Notecus type: DNA
A;Molecule type: DNA
A;Residues: 1-334 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35808.1; PID:g13361852; GSPDB:GN00154
A;Cross-references: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                     C;Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text_change 03-Aug-2001 C;Accession: A99927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: ynhG
C;Superfamily: conserved hypothetical protein b0819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, .A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:AE002014; A: evnorimental source: strain R1
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A; Residues: 1-277 <WHI>
A; Gene: ECs2385
C; Superfamily: conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ECs2385 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: ydiA protein
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                                                                                                                                                                A; Status: preliminary
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A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: F64925
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Best Local
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                                                                                                                                                                                                                                                                                  T.; Makino, K.; Ohnishi, M.; Yasunaga, T.; Kuhara, S.;
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7; Conser
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63.68;
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77.8%;
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    Mismatches

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Pred. No.
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protein b0819
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C;Superfamily: recombination protein recA
C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; nuclectide binding; P-loop;
F;68-75/Region: nuclectide-binding motif A (P-loop)
F;142-147/Region: nuclectide-binding motif B
                                                                                                                                                                                                                                                            Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72201
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L23425; NID:g385169; PIDN:AAA27417.1; PID:g385170 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Wetmur, J.G.: Wong, D.M.; Ortiz, B.; Tong, J.; Reichert, F.; Gelfand, D.H. J. Biol. Chem. 269, 25928-25935, 1994
A;Title: Cloning, sequencing, and expression of RecA proteins from three distantly relat A;Reference number: A55020; MUID:95014407; PMID:7929298
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                                                                                                                         C; Genetics:
                                                                                                                                             A;Cross-references: GB:AE001823; GB:AE000512; NID:g4982441; PIDN:AAD36921.1; PID:g498244
A;Experimental source: strain MSB8
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A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ynhG [imported] - Escherichia coli (strain O157:H7, substrain EDL93, C;Species: Escherichia coli
                                                                                                A; Gene: TM1859
                                                                                                                                          A; Experimental
                                                                                                                                                                                            A; Residues: 1-356 < ARN>
                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombination protein recA - Thermotoga maritima (strain MSB8)
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Best Local
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L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
409, 529-533, 2001
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nilarity 77.8%;
Conservative*
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Pred. No. 31;
0; Mismatches
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son, D.;
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  Search completed: January 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: C88445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Residues: 1-379 <STO>
A;Note: similar to ribosomal protein L3
A;Note: similar to ribosomal protein L3
                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: hypothetical protein D9476.2

C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S61154
                                                                                                                                                     A;Gene: SGD:GGA1; MIPS:VDR358w
A;Cross-references: SGD:S0002766
A;Map position: 4R
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC25H2.16c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein C2686.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88445
                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-557 < DUZ>
                                                                                                                                                                                                                                                                                                                             A; Reference number: S61148
A; Accession: S61154
                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL bata Library, June 1995 A:Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: C26E6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U28372; NID:g849170; PID:g849172; GSPDB:GN00004; MIPS:YDR358
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Best Local Similarity
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Best Local
523 ISVNLGKPIK 532
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                                    1 LSVRLGXPVK 10
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77.8%;
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Pred. No.
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Pred. No.
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Pred. No. 51;
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35;
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2003, 12:37:23

Job time : 16.1429 secs

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Result
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                             Score
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49
1 LSVRLGXPVKE 11
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  Gapop 10.0 , Gapext 0.5
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JSIDSZ/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*

JSIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*

JSIDSZ/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*

JSIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

JSIDSZ/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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572
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  AAB47795
AAM48266
AAM48267
AAR98144
AAR98145
AAW13863
AAW11572
AAW11525
AAW11525
AAW11524
                                         The DNA polymerase The DNA polymerase The DNA polymerase The DNA polymerase T. neapolitana The Thermotoga neapoli
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Native DNA
Native DNA
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neapoli
neapoli
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DNA	AAW83974	19	893	95.9	47
lymeras	AAW78758	19	893	95.9	47
	AAW11513	18	893	5	47
neapol	AAW13902	18	893	5	47
neapol	AAW13901	18	893	ÇI	47
	0	<u>ш</u>	893	95.9	47
toga nea	AAW13899	18	893	ŗ	47
son	AAR23146	μ ω	893	5	47
O	AAR21830	13	893	95.9	47
Mutant thermostab	AAR23148	13	875	5	47
Mutant thermostab	AAR23147	13	857	5	47
Mutant	AAR23149	13	821	5	47
Mutant Thermotoga	AAY33763	20	774	.5	47
Mutant thermostab	AAR23150	13	755	5	47
The DNA polymeras	AAW83972	19	700	5	47
The DNA polymeras	AAW78759	19	677	5	47
The DNA polymeras	AAW84003	19	674	5	47
The DNA polymeras	AAW84002	19	674	ŗ	47
Tne DNA	AAW84001	19	674	'n	47
The DNA polymeras	AAW84000	19	674	ĊŢ	47
The DNA polymeras	AAW83969	19	674	5	47
Mutant thermostab	AAR23151	<u>1</u> 3	611	5	47
The DNA polymeras	AAW83999	14	610	5	47
The DNA	AAW83977	19	610	5	47
DNA polymeras	97	19	610	5	47
olymera	152	18	610	ū	47
neapol	M	18	610	S	47
neapol	N	18	610	ū	47
neapol	AAW11519	18	610	ÇT,	47
neapol	$\mu$	18	610	5	47
	$\mathbf{H}$	18	610	5	47
	AAW11516	18	610	5	47
	-	18	610	S.	47
rmotoga neapol	$\mathbf{H}$	18	610	95.9	47
Tne DNA polymerase	AAW83971	19	609	5	47

## ALIGNMENTS

RESULT 1 AAB47795

AAB47795 standard; peptide; 11 AA

Native DNA polymerase motif #5

25-MAR-2002 AAB47795;

(first entry)

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Smith ES, Elfstrom CM, Gelfand DH, Schoenbrunner NJ, Wang AM;
                                                                                                                                                         Thermotoga sp.
                                                                                                                                                                           dye; amplification
                                                                                                                                                                                  DNA polymerase; reverse transcription; primer; divalent cation; mutant; transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                 18-APR-2000; 2000US-198336P.
                                                                  12-APR-2001; 2001EP-0109341.
                                                                                     07-NOV-2001
                                                                                                     EP1152062-A2
                                                                                                                                 Misc-difference
                               (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                  Location/Qualifiers
                                                                                                                       /label= Val, Ile
              Higuchi RG,
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RESULT 2
AAM48266
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate didexynucleotides labelled with fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction. This motif is derived from DNA polymerases from Thermotoga species maritima and neopolitana.
                                         Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       native forms of motifs derived from DNA polymerases used in to of the invention. The method for reverse transcribing an RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 4; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase \,
             Disclosure; Page 7; 23pp; English
                                                                                                                                             Smith ES, Elfstrom CM, Schoenbrunner NJ, Wang
                                                                                                                                                                                                                                                                                                 07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                 aye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Native DNA polymerase motif #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM48266 standard; Peptide; 11 AA
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                                                                                                             WPI; 2002-076891/11.
                                                                                                                                                                                                                               18-APR-2000; 2000US-198336P
                                                                                                                                                                                                                                                                12-APR-2001; 2001EP-0109341
                                                                                                                                                                                                                                                                                                                                  EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2002
                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                               transverse transcription reaction; fluorescein; cyanine; thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                               amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVRIGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ng a transverse transcription reaction mixture which comprises the primer, a divalent cation, and a mutant thermoactive DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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100.0%;
                                                                                                                                                                Gelfand DH,
                                                                                                                                               AM;
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                                                                                                                                                             Higuchi RG,
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. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
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                                                                                                                                                              Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 3
AAM48267
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase's ability to incorporate dideoxynucleotides labelled fluorescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating a transverse conserve. and a mutant thermoactive DNA RNA, a primer, a divalent cation, and a mutant thermoactive DNA polymerase. These mottis represent a conserved region which affects the polymerase. These mottis represent a conserved region which affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises
                                                                                                                                                                                      Reverse transcribing an RNA, comprises performing a reverse transcriptase polymerase chain reaction amplification of a mixture using a mutant thermoactive DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transverse transcription reaction; fluorescein; cyanine; dye; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48267 standard; Peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides taster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating a transverse transcription reaction mixture which comprises the
                                                                                                                                                                                                                                                          WPI; 2002-076891/11.
                                                                                                                                                                                                                                                                                         Schoenbrunner NJ, Wang AM;
                                                                                                                                                                                                                                                                                                            Smith ES, Elistrom CM,
                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                           18-APR 2000; 20000S 1983361
                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2001; 2001EF 0109341
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1152062-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; reverse transcription; primer; divalent cation; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Native DNA polymerase motif #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     needed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reverse transcription extension rates, and consequently less time is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSVRLGVPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.98;
90.98;
                                                                                                                                                                                                                                                                                                            Gelfand DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 23;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                          Higuchi RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                          Myers TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermoactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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The sequences given in AAB47791-97 and AAM48259-AAM48270 represent the native forms of motifs derived from DNA polymerases used in the method of the invention. The method for reverse transcribing an RNA, comprises of the invention. The transcription reaction mixture which comprises the transcription of the following a transverse transcription reaction mixture which comprises the

Disclosure; Page 7; 23pp; English.

polymortase. These motifs represent a conserved region which affects the DNA polymerase's ability to incorporate dideoxymucleotides labelled with thucrescein and cyanine family dyes. The method of the invention is useful in reverse transcription/amplification reactions. The method

RNA, a primer, a divalent cation, and a mutant thermoactive DNA

B

78

LSVRLGIPVKE 88

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RESULT 4
AAR98144
                                            Query Match
Best Local Similarity
Thehes 10; Conserve
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                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provides improved reverse transcription efficiency at lower enzyme concentrations relative to previous high temperature reverse transcription methods, and provide a wider range of usable salt concentrations. The use of the mutant DNA polymerase provides faster reverse transcription extension rates, and consequently less time is needed for the reaction.
                                                                                                                                                                                                                                                                                                                                       The C-terminal portion (AAR98144) of the 100 kDa thermostable DNA polymerase (AAR98143) of Thermotoga neapolitana (Tne) includes an O helical region. Tna polymerase is a thermostable enzyme suitable for use in DNA sequencing and amplification reactions. It can be obtd. from host cells, e.g. E. coli, carrying the DNA polymerase gene. Mutants having improved enzymatic properties may also be produced (see also AAR98144-47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga neopolitana DNA polymerase and thermostable mutants useful in DNA sequencing and amplification reactions % \left( 1\right) =\left( 1\right) +\left( 1\right)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT30049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotoga neapolitana strain DSM 5068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA polymerase; Tne; DNA sequencing; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tne DNA polymerase C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98144 standard; Protein; 230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; Fig 5A-B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-209362/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO961064∩-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermostable enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSVRLGXPVKE 11
1 LSVRLGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                       230 AA;
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0316423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0370190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US12358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 63..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= O-helical_region
                                                                                                                           95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.98;
90.98;
                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                    Score 47; DB 17; Length 230; Pred. No. 0.094; 0; Mismatches 1; Indels
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Pred. No. 0.0033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                        9.
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                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Site-directed mutagenesis was used to substitute a tyrosine residue for phenylalanine in the O-helical region of Thermotoga neapolitana (The) DNA polymerase. This residue corresponds to position 67 of a C-terminal frayment (see also ANR98144) of the enzyme. As a result of the mutation, the polymerase becomes non-discriminating against non-natural nucleotides such as dideoxynucleotides. The mutant enzyme, which may also incorporate a D323A mutation in the N-terminal portion (see ANR98147), is active and theat stable, and can be used in DNA sequencing and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-1995;
30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase;
thermostable en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 50; Fig5A-B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotoga neopolitana DNA polymerase and thermostable mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chatterjee DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09610640-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The DNA polymerase C-terminal region (F67Y mutant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-1996
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                                                       AAW13863;
                                                                                                   AAW13863 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFE
                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                             1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1996-209362/21
                                                                                                                                                                                                                                         LSVRLGIPVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in DNA sequencing and amplification reactions
                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 AA;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               se; Tne; DNA sequencing; amplification;
enzyme; protein engineering; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0370190
94US-0316423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US12358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers 63..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- O-helical_region
                                                                                                                                                                                                                                         88
                                                                                                   Protein; 230
                                                                                                                                                                                                                                                                                                                                                                        95.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 17
Pred. No. 0.094;
                                                                                                      Ą
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplification;
                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                            Length 230;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                             Caps
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AAY51572
ID AAY5
XX
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 PN XXX XXX AC
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                          Query Match
Best Local :
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02-OCT-1995;
02-OCT-1995;
21-DEC-1995;
                                                                                                                                                                                                                                                                                       single reading frame. The 3 sequences were compared with known polymerase amino acid sequences and spliced to generate the Tne sequence given in AAW13863. A complete amino acid sequence for polymerase is given in AAW13899.
                                                                                                                                                                                                                                                                                                                             Polypeptide sequences (AAW13862-64) were deduced for all 3 reading frames of a DNA sequence (AAT60031) encoding the C-terminal region, including the O-helix, of the Thermotoga neapolitana (Tne) DNA polymerase. Frameshift errors generated during sequencing of the DNA prevented the entire amino acid sequence being deduced from a
                                                                                                                                                                                                                                                                                                                                                                                                          Mutant DNA polymerase, esp. from Thermotoga - has reduced exonuclease activity or dideoxynucleotide discrimination, useful for DNA amplification, synthesis and sequencing
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chatterjee DK, Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-15.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9709451-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga neapolitana
 18-JAN-2000
                   US6015668-A.
                                    Thermotoga neapolitana
                                                                                                        18-MAY-2000
                                                                                                                                             AAY51572 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT60031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHAT/) CHATTERJEE D K. (HUGH/) HUGHES A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme engineering; protein engineering; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA polymerase; Tne; exonuclease; DNA amplification; DNA sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The DNA polymerase C-terminal region
                                                                  DNA polymerase; PolI; O-helix; DNA sequencing; amplification; mutant;
                                                                                   T. neapolitana Tne polymerase C-terminal protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 5; 120pp; English.
                                                       thermostability; Tne
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                             78 LSVRLGIPVKE 88
                                                                                                                                                                                                               1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-192925/17
                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                        230 AA;
                                                                                                                                                                                                                                   Conservative
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0537397.
95US-0537400.
95US-0576759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US14189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0525057
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                                                                                                                                                                                                                                           95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain DSM 5068
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                           Score 47; DB 18
Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                    A complete amino acid sequence for "I'ne
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                    Length 230;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                        δÃ
                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                 Sequence
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YX
PR
PR
PR
PR
PR
PR
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-1995;
08-SEP-1995;
02-OCT-1995;
21-DEC-1995;
14-AUG-1996;
dideoxynucleotides (ddWTP). They permit sequencing at high temperature; provide strong, clear sequences (increased signal-to-noise ratio); can sequence more than 500 bases; reduce false stops in the sequence ladder; reduce template requirements 10-fold (when using 350 labeling); and also requirements for primer and labeled terminator. They increase sequencing efficiency with structure-containing or GC-rich templates; reduce film exposure times; do not generate sequencing artefacts with homopolymeric sequences and allow quantitation of bases in heterologous mixtures. This sequence represents the Thermotoga neapolitana The polymerase carboxyl terminal which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                        sequencing, amplification and synthesis of DNA by essentially standard methods, also for DNA labeling and for synthesis of CDNA from mRNA templates. (1) have higher thermostability than known enzymes (e.g. 50% retention of activity after 60 min at 90 plusoC), and may be free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing, amplification and synthesis methods, using mutant forms of Thermotoga neapolitana polymerase with reduced exonuclease activity or reduced discrimination against dideoxynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-181138/16.
N-PSDB; AAZ88767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded DNA or synthesizing DNA which use a mutant Thermon neapolitana DNA polymerase (I) or its fragments. (I) are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Column 53-54; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                        of exonuclease activity and/or ability to discriminate against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel methods for sequencing DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chatterjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0706706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0689818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0537400
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95US-0370190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga
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230 AA;
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Query Match
Best Local Similarity
 AAW11525
                                                78 LSVRLGIPVKE 88
                                                                  1 LSVRLGXPVKE II
                                                                                      10;
standard;
                                                                                    Conservative
 Protein;
                                                                                              95.98;
90.98;
                                                                                    Score 47; DB Pred. No. 0.09
0; Mismatches
494
                                                                                              0.094;
                                                                                                       DB 21;
                                                                                                       Length 230;
                                                                                      Indels
                                                                                     0;
                                                                                     Gaps
                                                                                      0;
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## AAW11525;

15-APR-1997

(first entry)

Thermotoga neapolitana DNA polymerase Tne M284 delB

DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana

Synthetic.

W09641014-A1

19-DEC-1996

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В
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                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                  Deletion mutant The M284 delB (AAW11525) of the The DNA polymerase (see also AAW11513) of Thermotoga neapolitana lacks the N-terminal 283 amino acids from the 5' exonuclease domain of the native enzyme and also has amino acid residues 309-424 of the 3' exonuclease domain deleted. It can be obtd. by expression of a DNA construct (AATS8155) created by restriction digestion of pM284 derived DNA also AAT58135). When expressed in E. coli, The M284 delB showed no detectable polymerase activity. In contrast, a The M284 mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolchakova E, Har....
NR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1996;
07-JUN-1995;
        WPI; 1997-052374/05
N-PSDB; AAT58145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable DNA polymerase from Thermotoga neapolitana - \mathtt{DNA} sequencing or for amplification of double stranded \mathtt{DNA}
                               Bolchakova E, Hartnet Slater MR, Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT58155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                                                      31-MAY-1996;
07-JUN-1995;
                                                                                              07-JUN-1996;
                                                                                                                                                                                                                          AAW11524;
                                                                                                                                                                                                                                          AAW11524 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 174-175; 200pp; English.
                                                      (PROM-) PROMEGA CORP.
                                                                                                              19-DEC-1996
                                                                                                                             WO9641014-A1
                                                                                                                                            Synthetic
                                                                                                                                                            polymerase chain
                                                                                                                                                                     thermostability;
                                                                                                                                                                           DNA polymerase; Tne;
                                                                                                                                                                                           Thermotoga neapolitana DNA polymerase The M323 mutant
                                                                                                                                                                                                           15-APR-1997
                                                                                                                                                                                                                                                                                342
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                               (see also
                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                              1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-052374/05
                                                                                                                                                                                                                                                                                LSVRLGIPVKE 352
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                              AAW11514) was active.
                                                                                                                                                                                                                                                                                                                                             494 AA;
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hartnett JR,
                                                                      96US-0656664.
95US-0484661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0656664
95US-0484661
                                       Hartnett
                                                                                              96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US09641
                                                                                                                                                            DNA sequencing; amplification; PCR; reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                           entry)
                                                                                                                                                                            thermostable enzyme; protein engineering;
                                                                                                                                                                                                                                                                                                                       95.9%;
                                        JR,
                                                                                                                                                                                                                                          572
                                                                                                                                                                                                                                                                                                                      Score 47;
Pred. No. (
                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang
                                       Huang
                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                Mismatches
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                                       'n
                                                                                                                                                                                                                                                                                                                        0.22;
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                                        Miller KM,
                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                                                                               Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otto
                                        Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                        φ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ָטי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                0;
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                     Example 3; Page 133-135;
                                                                                                                                                            Bolchakova E,
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Query Match
Best Local
                                                                                                                                                                                           using a DNA construct (AAT58145) created by restirction enzyme digestion. When expressed in E. coli, The M323 produced no detectable polymerase activity. In contrast, a The M284 mutant
                                                                                                                                                                                                                                                                              Deletion mutant The M323 (AAW11524) of Thermotoga neapolitana DNA polymerase The (see also AAW11513) has an artificially created methionine at amino acid position 323 as the initiator methionine in the 3' exonuclease domain of the enzyme. It can be expressed in the 3' exonuclease domain of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequencing or for amplification of double stranded DNA
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 169-175; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                    (see also AAW11514) was active.
l Similarity
10; Conserv
                                                                                                               572 AA;
                             95.98;
90.98;
                             Score 47;
Pred. No.
                                0
                                                          B
                                . 26;
                                                       18;
  1;
                                                    Length
0;
Gaps
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AAW11523 standard; Protein; 578 AA
                                                                                                                                                                                      419 LSVRLGIPVKE 429
                                                                                                                                                                                                                             1 LSVRLGXPVKE 11
(first entry)
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Conservative

0; Mismatches

Indels

0,

DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana Thermotoga 15-APR-1997 AAW11523; DNA polymerase Tne M316 mutant

07-JUN-1996; Synthetic. 19-DEC-1996 W09641014-A1 96WO-US09641

31-MAY-1996; 07-JUN-1995; (PROM-) PROMEGA CORP 9505-0656664. 9505-0484661.

Hartnett

JR,

Huang F,

Miller KM,

Otto

סי

Thermostable DNA polymerase from Thermotoga neapolitana - DNA sequencing or for amplification of double stranded DNA N-PSDB; AAT58144. 1997-052374/05 Storts DR; useful

200pp; English.

in

mutagenesis. When expressed in E. coli from a T/ or The M316 produced no detectable polymerase activity. mutant (see also AAW11514) was active. methionine at amino acid position 316 as the initiator methionine. It can be expressed using a DNA construct (AATS8144) created by introducing a Met residue at position 316 (and a corresponding NCOI site) into the native gene (AATS8134) via site-directed mutagenesis. When expressed in E. coli from a T7 or trc promoter. Deletion mutant Tne M316 (AAW11523) of Thermotoga neapolitana DNA polymerase Tne (see also AAW11513) has an artificially created A Tne M284

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
amplifying the fragment, followed by analysis, identification or typing of the amplicons. The DNA polymerases used are thermostable and the modification or mutation is in the O-helix of the The DNA polymerase. Analysis of polymorphic DNA is particularly used to establish relationships between individuals (forensic or paternity testing), particularly where the polymorphism is a mini- or micro-satellite or short tandem repeat. More generally the DNA polymerase and its mutant form are useful in any process that involves nucleic acid amplification, e.g. identification of pathogens, cancer or genetic diseases (cystic fibrosis, haemophilia, Alzheimer's disease), screening organs or tissues before transplanting, diagnosis, plant breeding.

Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Tne DNA polymerase sequence
                                                                                                                                                                                         Sequences AAW83969 to AAW84011 represent The (Thermotoga neapolitana) DNA polymerase mutants which can be used in the method of the invention of identifying and analysing polymorphic DNA. The method comprises reacting a DNA sample with at least one DNA polymerase having reduced ability to add non-templated nucleotides to the 3'-terminus and amplifying the fragment, followed by analysis, identification or typing of the amplicons. The DNA polymerases used are thermostable and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tne; O-helix; DNA polymerase; polymorphic; amplicon; thermostable; mutant; forensic; paternity testing; nucleic acid amplification; cancer pathogen; genetic disease; cystic fibrosis; haemophilia; transplanting; Alzheimer's disease; screening; organ; diagnosis; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW83971;
                                                                                                                                                                                                                                                                                                                                  Claim 52; Page -; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                               New mutant polymerases that do not add non-templated 3^\prime-nucleotides - specifically for analysis of hypervariable polymorphisms e.g. for forensic and paternity testing, disease diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chatterjee DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1998;
07-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09835060-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tne DNA polymerase mutant N'del284, D323A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW83971 standard; Protein; 609 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-447254/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 LSVRLGIPVKE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LSVRIGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0037393.
97US-0037393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US02791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=_"wild-type Asp is replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= D323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                  neapolitana. The naturally-occurring Met-284 residue becomes the initiating methionine. The mutant enzyme is obtd. by expression of DNA clone pM284 (AAT58135) produced by restriction enzyme digestion of the native gene (AAT58134). The N-terminal deletion eliminates the 5' exonuclease activity of the enzyme. The M284 has a half-life at 97.5 deg C of 18 min compared with 5 min for the native enzyme. Amino acid substns. in the 3' exonuclease domain of The M284 (see also AAM11516-22) yield enzymes ess. suitable for DNA
                                                                                                                                                                                                                                                                                                                                                      31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase; The; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR; polymerase chain reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga neapolitana DNA polymerase Tne M284 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW11514 standard; Protein; 610 AA
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                                                                                                                              DNA polymerase mutant Tne M284 (AAW11514) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga
                                                                                                                                                                      Claim 11; Page 128-131; 200pp;
                                                                                                                                                                                                Thermostable DNA polymerase from Thermotoga neapolitana - DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                         WPI; 1997-052374/05
                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
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                                                                                                                                                                                                                                            N-PSDB; AAT58135
                                                                                                                                                                                                                                                                                    Slater MR,
                                                                                                                                                                                                                                                                                                 Bolchakova E,
                                                                                                                                                                                                                                                                                                                           (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVRLGIPVKE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609
                                                                                                                                                                                                                                                                                   Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                Hartnett JR,
                                                                                                                                                                                                                                                                                                                                                    96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                              96WO-US09641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15..199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /!abel= Polymerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= 5'-Exonuclease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= 3'-Exonuclease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 1
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                Huang F,
                                                                                                                                                                      English.
                                                                                                                                                                                                   of double stranded DNA
                                                                                                                                                                                                                                                                                                Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                 Otto
                                                                                                                                                                                                                useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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sequencing and amplification reactions, e.g.

PCR.

DЬ

Query Match

DB 18;

Length 610;

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RESULT 13
AAW11515
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                       DNA polymerase mutant The M284(D323E) (AAW11515) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga neapolitana and contains a D323 substn. in the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAT58136) created by site-directed mutagenesis of construct pM284 (see also AAT58135). The M284(D323E) has no significant 5' or 3' exonuclease activity and has a half-life at 97.5 deg c of 12.5 min compared with 5 min for native The and 8 min for native Taq. It can be used in DNA sequencing reactions and for the amplification of double stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW11515 standard; Protein; 610 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                              Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase; Tne; thermostability; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW11515;
                                                                                                                                                                                                                                        N-PSDb; AAT58136
                                                                                                                                                                                                                                                                                        Bolchakova E,
                                                                                                                                                                                                                                                                                                                                          31-MAY-1996;
07-JUN 1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga neapolitana DNA polymerase The M284(D323E) mutant.
Sequence
                                                                                                                                                                                                                                                                                                                  (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9641014-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 LSVRLGIPVKE 468
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                                                                                                                                                                                                                                                   1997-052374/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                    Page 138-140; 200pp; English.
 610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610
                                                                                                                                                                                                                                                                              Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                        Hartnett
                                                                                                                                                                                                                                                                                                                                          96US-0656664
95US-0484661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                  96WO-US09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15..199 *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tne; thermostable enzyme; protein engineering;
DNA sequencing; amplification; PCR;
reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "the D323E substn. corresponds to amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Polymerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- 3'-Exonuclease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        = 5'-Exonuclease_domain
"residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                         JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid position 40 in the mutant enzyme'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 18;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                         Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                         Miller KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>د ـ ـ و</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                         01.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                             in
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RESULT 14
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Matches
                mutagenesis of construct pM284 (see also AAT58135). The M284(\mu3) has no significant 5' or 3' exomuclease activity and has a half-life at 97.5 deg C of 5 min (unchanged from the native enzyme). It can be used in DNA sequencing reactions and for the
                                                                                                       DNA polymerase mutant The M284(D325D) (AAWI1516) lacks the N-terminal 283 amino acid residues of the mative enzyme (AAWI1513) of Thermotoga neappolitana and contains a E325D substn. in the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAT58137) created by site-directed expression of a DNA clone (AAT58137) created by site-directed
                                                                                                                                                                                                                                              Claim 11; Page 142-144; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT58137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW11516 standard; Protein; 610 AA
amplification of double stranded
                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Slater
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolchakova E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROM:) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase chain reaction; exonuclease; Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermotoga Reapolitana DNA polymerase Tne M284(E325D) mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW11516;
                                                                                                                                                                                                                                                                                                             Thermostable DNA polymerase from Thermotoga neapolitana - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doma i n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermostability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase; Tne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSVRLGXPVKE 11
                                                                                                                                                                                                                                                                                             sequencing or for amplification of double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSVRLGIPVKE 468
                                                                                                                                                                                                                                                                                                                                                                                    1997-052374/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MR,
                                                                                                                                                                                                                                                                                                                                                                                                                              Storts DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bartnett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0656664
95US-0484661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- 5'-Exonuclease_domain
/note= "residues 1-14 comprise the C-terminal
end of the The 5'-exonuclease domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Polymerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200..610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fne; thermostable enzyme; protein
DNA sequencing; amplification; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.98;
90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "the E325D substn. corresponds to amino acid position 42 in the mutant enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      . X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB Pred. No. 0.27 0; Mismatches
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reactions
DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller KM,
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                                                                                       Tne M284 (H325D)
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Sequence

610 AA;

XX Ld XX Vd

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RESULT 15
AAW11517
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Best Local Similarity
                                    DNA polymerase mutant The M284(Y464F) (AAW11517) lacks the N-terminal 283 amino acid residues of the native enzyme (AAW11513) of Thermotoga neapolitana and contains a Y464F substn. in the 3' exonuclease domain (numbering according to the native enzyme). It is obtd. by expression of a DNA clone (AAT58138) created by site-directed mutagenesis of construct pM284 (see also AAT58135). The M284(Y464F) has no significant 5' exonuclease activity and only 1.9% of the native 3' exonuclease activity. Its half-life at 97.5 deg C is 16 min compared with 5 min for native The and 8 min for native Taq. It can be used in DNA sequencing reactions and for the
                                                                                                                                                                                                                                                                     WPI; 1997-052374/05.
N-PSDB; AAT58138.
                                                                                                                                                                                                                                                                                                         Bolchakova E, Hartnet Slater MR, Storts DR;
                            amplification of double stranded DNA.
                                                                                                                                                                                              Claim 11; Page 147-149; 200pp; English.
                                                                                                                                                                                                                          Thermostable DNA polymerase from Thermotoga neapolitana - useful DNA sequencing or for amplification of double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; Tne; thermostable enzyme; protein engineering; thermostability; DNA sequencing; amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW11517 standard; Protein; 610 AA
Sequence
                                                                                                                                                                                                                                                                                                                                                      (PROM-) PROMEGA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga neapolitana DNA polymerase Tne M284(Y464F) mutant.
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 610 AA;
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95US-0484661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= 3'-Exonuclease_domain
/note=."the Y464F substn. corresponds to amino
acid position 181 in the mutant enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 5'-Exonuclease_domain
/note= "residues 1-14 comprise the C-terminal
end of the Tne 5'-exonuclease domain"
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Query Match 95.9%; Score 47; DB 18; Length 610; Best Local Similarity 90.9%; Pred. No. 0.27; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps Oy 1 LSVRIGXPVKE 11

Db 458 LSVRLGIPVKE 468
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Search completed: January 15, Job time: 29.2857 secs

2003, 11:20:17

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-891-332A-3

US-09-891-332A-2

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US-09-891-332A-9

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US-09-891-332A-9
     US-09-741-664-2
US-10-053-632-4
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US-09-823-649A-15
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Sequence 5, Appli
Sequence 16, Appli
Sequence 4, Appli
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  RESULT 2
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Best Local (
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                                                                                                                                                                                                                                                      Similarity
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61.2		61.2			61.2		61.2	63.3		63.3	63.3		63.3	63.3	65.3	69.4	69.4	73.5	83.7	83.7	83.7	83.7	83.7	83.7	83.7
471	471	408	403	390	301	102	95	259	259	250	189	159	114	96	319	676	666	30	610	11	11	11	11	11	<u> </u>
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US-09-761-640-4	US-09-955-732-21	US-09-761-640-6	US-09-738-626-6217	US-09-815-242-11146	US-09-738-626-4278	US-10-001-857-189	US-09-895-913A-266	US-09-815-242-11603	US-09-991-211-3	US-10-027-559-6	US-09-216-393-130	US-09-867-550-954	US-09-809-545A-74	US-09-867-550-952	US-09-738-626-6900	US-09-815-242-13513	US-09-815-242-13637	US-09-922-261-34	US-09-891-332A-10	US-10-052-417-17	US-10-052-417-16	US-10-052-417-15	US-10-052-417-6	US-10-052-417-5	US-10-052-417-4
-	21,	Sequence 6, Appli	Sequence 6217, Ap	Sequence 11146, A			Sequence 266, App	Sequence 11603, A		Sequence 6, Appli		954	74,		О.		136	Sequence 34, Appl	Sequence 10, Appl	17,	16,	5	σ,	ų,	Sequence 4, Appli

## ALIGNMENTS

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; OTHER INFORMATION: X is V or I US-09-823-649A-5
                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09823649A Patent No. US20020012970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Elfstrom, Carita APPLICANT: Gelfand, David APPLICANT: Hiquchi
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYME FILE REFERENCE: RPA1006 CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT PILLING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DAPE: 2000-04-18
                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence motif
                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers, Thomas
Schoenbrunner, Nancy
    Conservative
                  95.9%; Score 47;
100.0%; Pred. No.
0; Mismatches
                  DB 10; I
                                  Length 11;
Indels
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RESULT 4
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Sequence 4, Application US/09891332A Patent No. US20020168646A1 GENERAL INFORMATION:
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LENGTH: 11
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020012970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.9%;
Best Local Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09823649A
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18 NUMBER OF SEQ LD NOS: 21 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS FILE REF RENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,649A CURRENT ETLING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/198,336 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Higuchi, Russell APPLICANT: Myers, Thomas APPLICANT: Schoenbrunner, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smith, Edward APPLICANT: Elfstrom, Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Smith, Edward
                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Thermotoga neapolitana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERAS
FILE REFERENCE: RPA1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Alice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                           Local Similarity hes 10; Conservat
                                                                                                                                                      1 LSVRLGXPVKE 11
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                                                                                                                                    LSVRLGIPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elfstrom, Carita
Gelfand, David
Higuchi, Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schoenbrunner, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers, Thomas
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                            95.9%; Score 47; DB 10; Length 11; 90.9%; Pred. No. 0.00037;
                                                                                                                                                                                                             0;
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Pred. No. 0.00037;
                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                           0;
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                                                                                                                                                                                                           Gaps
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RESULT 5
US-09-891-332A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 LSVRLCTPVKE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LSVRLGXPVKE 11
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32.893
REFERENCE/DOCKET NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAA: 202-371-2540
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                      Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                            COUNTRY: USA
                                                                                                STATE: DC
                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                          Application US/09891332A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 610 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/019,160 FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/891,332A
FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                    Chatterjee, Deb K.
                                                                                                                                                                                                                                                                      Solus, Joseph
Yang, Shuwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.9<del>8</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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1; Indels Length 708;

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Gaps

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US-09-891-332A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                           APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1-0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0942.4250002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 677 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                              APPLICATION NUMBER: 09/019,160 FILING DATE: <Unknown>
                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                    APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.H.L.C STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/019,160
    REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang, Shuwei
                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.9%;
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Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                           US-09-891-332A-2
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  Query Match
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                                                                                                                                                                                           TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SPO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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                                                         MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0942.4250002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                   NAME: ESMOND, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                       TOPOLOGY: not relevant
                                                                                                                            STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/037,393
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLING DAFFE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPELICATION NUMBER: 09/019,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
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TELEFAX: 202-371-2540
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                                                                                                                                                                      LENGTH: 893 amino acids
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90.9%;
95.9%;
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Score 47;
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DB 9;

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US-09-891-332A-7
Sequence 7, Application US/09891332A
Patent No. US20020168646A1
CENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                      Local Similarity
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TOTAL
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
            APPLICANT: Chatterjee, Deb K. Solus, Joseph
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/019,160
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
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STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 893 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3934
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                      Score 47; DB 9; Pred. No. 0.052;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                       Length 893;
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US-09-891-332A-8
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                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09891332A Patent No. US20020168646A1 GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N.W., Suite 600
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N.W., Suite 600
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TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
                                                                                                                                                                                                                                TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                ZIP:
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FILING DATE: CUDKINGWN>
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
                                                                                                   COUNTRY:
                                                                                                                         STATE: DC
                                                                                                                                        CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0942.4250002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
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                                                                                  20005-3934
                                                                                                                                                                                                                                                                                                Solus,
                                                                                                                                                                                                                                                                                  Yang,
                                                                                                     USA
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90.98;
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Pred. No. 0.052;
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Sequence 9, Application US/09891332A Patent No. US20020168646A1 GENERAL INFORMATION:
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Best Local Similarity
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TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                          ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,160
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solus, Joseph Solus, Joseph Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic Nucleic Acid Fragments and Uses Thereof
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
SLQUENCE DESCRIPTION: SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                    NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                              APPLICATION NUMBER: US/09/891,332A FILING DATE: 27-Jun-2001
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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                                                                                                APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/037,393 FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0942.4250002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.9%;
90.9%;
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                                                                                                                                                      US-09-741-664-1
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US-09-741-664-1
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Patent No. US20010041334A1
PARREL INFORMATION:
                                                                            Matches
                                                                                                Best
                                                                                                                Query Match
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APPLICANT: Solus, Joseph
TITLE OF INVENTION: Stable Compositions for Nucleic Acid
TITLE OF INVENTION: Sequencing and Amplification
MUMBER OF SPOUSNCES: 2
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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741 LSVRLGIPVKE 751
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                                                                          Local Similarity nes 10; Conserv
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                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    1 LSVRLGXPVKE 11
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LENGTH: 893 amino acids
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                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                            893 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                          Conservative
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90.98;
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                                                                                                                                                                                                                                                                                                                                                             32,893
                                                                        0; Mismatches
                                                                                          Score 47; DB 10; Length 893; Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                            0942.3910000
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US-09-891-332A-9

US-09-891-332A-8

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US-10-053-632-4
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US-09-741-664-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20010041334A1 GENERAL INFORMATION:
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                                     APPLICANT: Sigua, Chris
APPLICANT: Myers, Thomas
TITLE OF INVENTION: THERMOSTABLE DNA PLOYMERASES INCORPORATING NUCLEOTIDE TRIPHOSPHAN
TITLE OF INVENTION: LABELED WITH FLUORESCEIN FAMILY DYES
TILE REFERENCE: 1803-339-999
CURRENT APPLICATION NUMBER: US/10/053,632
CURRENT FILING DATE: 2002-01-17
                                                                                                                                                                                      APPLICANT: Gelfand, David
APPLICANT: Kalman, Lisa
APPLICANT: Reichert, Fred
NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn version
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APPLICANT: Solus, Joseph
TITLE OF INVENTION: Stable Compositions for Nucleic Acid
TITLE OF INVENTION: Sequencing and Amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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Local Similarity 90.9%;
les 10; Conservative
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REFERENCE/DOCKET NUMBER: 09
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  version 3.0
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Query Match
Best Local Similarity
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US-10-053-632-5
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Search completed: January 15, 2003, 12:39:51 Job time: 10.8571 secs
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                                                                                                                                                                                                                    ; LOCATION: (4)...(4) ; OTHER INFORMATION: Xua at position 4 is any amino acid US-10-053-632-5
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; Patent No. US20020095560A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Siqua, Chris
APPLICANT: Myers, Thomas
TITLE OF INVENTION: THERMOSTABLE DNA PLOYMERASES INCORPORATING NUCLEOTIDE TRIPHOSP
TITLE OF INVENTION: LABELED WITH FLUORESCEIN FAMILY DYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gelfand, APPLICANT: Kalman, APPLICANT: Reicher
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1803-329-999
CURRENT APPLICATION NUMBER: US/10/053,632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Sequence from mutant OTHER INFORMATION: thermostable DNA polymerase NAME/KEY: VARIANT LOCATION: (4)..(4)
OTHER INFORMATION: Xaa at position 4 is any amino acid except glutamic acid resid NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
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                                                                                                        1 LSVRLGXPVKE 11
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                                                                     1 LSVXLGVPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalman, Lisa
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David
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                                                                                                                                                              83.7%;
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Pred. No.
                                                                                                                                                            Score 41; DB 12;
Pred. No. 0.0068;
                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0068
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                                                                                                                                                                           Length 11;
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                                                                                                                                            Indels
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Sequence:

Run on:

35, Appl 54, Appl

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                   Score
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49
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   Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                   Length DB
   US-08-537-400-16
US-08-706-702-18
US-08-706-706-706-18
US-08-484-661A-39
US-08-484-661A-37
US-08-484-661A-11
US-08-484-661A-11
US-08-484-661A-11
US-08-484-661A-11
US-08-484-661A-12
US-08-484-661A-13
US-08-484-661A-13
US-08-484-661A-23
US-08-484-661A-23
US-08-484-661A-23
US-08-484-661A-23
US-08-484-661A-35
US-08-656-664-8
US-08-656-664-23
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(without alignments)
34.855 Million cell updates/sec
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Sequence 11, Appl
Sequence 16, Appli
Sequence 19, Appli
Sequence 23, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 29, Appl
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18, Appl
19, Appl
39, Appl
39, Appl
39, Appl
37, Appl
37, Appl
37, Appl
37, Appl
37, Appl
37, Appl
31, Appl
  Query Match
Best Local Similarity
Watches 10; Conserve
                                                           ; MOLECULE TYPE: protein US-08-537-400-16
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US-08-537-400-16
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; Patent No. 5939301
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 09-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                            TYPE: a
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                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/537,400 FILING DATE: 02-OCT-1995 CLASSIFICATION: 435
                                                                                                                                         TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                             REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
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                                                                                            i: 230 amino acids
amino acid
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             Conservative
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PCT-US96-09641-16
PCT-US96-09641-29
PCT-US96-09641-29
PCT-US96-09641-29
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-39
PCT-US96-09641-34
US-09-019-160-5
US-09-019-160-5
US-08-48-819-4
US-08-48-819-4
US-08-706-702-3
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US-08-656-664-54
US-09-019-160-4
             0;
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         Score 47; DB 2; Pred. No. 0.012; 0; Mismatches
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                                  Length 230;
            Indels
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Sequence 16, Appli
Sequence 16, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 33, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
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Result No.

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WS-08-706-706-18

S-08-706-706-18

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US-08-706-702-18
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                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 02-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: US. APPLICATION NUMBER: US.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cloned DNA Polymerases from TITLE OF INVENTION: maritima and Mutants Thereof NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                 78
                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                1 LSVRLGXPVKE 11
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                                                                                               LSVRLGIPVKE 88
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                                                                                                                                                              10;
                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                             230 amino acids
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                                                                                                                                                                                                                                                                                                                                                              202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1995
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                                                                                                                                                                              95.9%;
90.9%;
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                                                                                                                                                                              Score 47; DB 2; Pred. No. 0.012;
                                                                                                                                                              Mismatches
                                                                                                                                                                                           Length 230;
                                                                                                                                                              Indels
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RESULT 4
US-08-484-661A-39
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Chatterjee, Deb K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                              78 LSVRLGIPVKE 88
                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 New York Ave., N.W., Suite
                                                                                           1 LSVRLGXPVKE 11
                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                           l Similarity
10; Conserv
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                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                             Esmond, Robert W.
                                                                                                                                                                                                                                                  240 amino acids
                                                                                                                                                                                                                                                                                                    202-371-2540
                                                                                                                           Conservative
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                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1996
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                                                                                                                                        95.98;
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                                                                                                                                      Score 47; DB 3;
Pred. No. 0.012;
                                                                                                                           Mismatches
                                                                                                                                                      Length 230;
                                                                                                                         Indels
                                                                                                                         0;
                                                                                                                       Gaps
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Sequence 39, Application US/08484661A Patent No. 6001645
GENERAL INFORMATION:

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APPLICANT:

SLATER, MICHAEL R. HARTNETT, JAMES R.

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Gaps

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US-08-656-664-39
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/08656664 Patent No. 6077664
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                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: BOICHAKOVA
TITLE OF INVENTION: N
TITLE OF INVENTION: N
UMBER OF SEQUENCES:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTOLNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 LSVRLGIPVKE 352
                APPLICATION NUMBER:
                                                                                                                                        COUNTRY: UZIP: 94104
                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll STREET: 220 Montgomery Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity tes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
OGY: linear . . .
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                                                                                                                                                                         California
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                                                                                                                                                                                                                                                                                                                  Otto, Paul
                                                                                                                                                                                                                                                                                                                                 Storts,
                                                                                                                                                                                                                                                                                                                                              Bolchakova, Elena
                                                                                                                                                                                                                                                                                                                                                                  Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                     Huang,
                                                                                                                                                                                                                                                                                                                                                                                                   Slater, Michael R
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                                                                                                                                                      United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLEN & CARROLL
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                                                                                                                                                                                                                                                                                                                               Douglas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODIFIED THERMOPHILIC DNA POLYMERASES FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.9%; Score 47; DB 3; 90.9%; Pred. No. 0.029;
              US/08/656,664
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                                                                                                                                                                                                            Suite 2200
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PCT-US96-09641-39
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95.9%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                     TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/09641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                       PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                          NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                              amino acid
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                                                                                                                                                 494 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States Of America
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Bolchakova, Elena
Storts, Douglas R.
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                                                                                                                                                                                                                       (415) 705-8410
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N: 435
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                                                                                                                                                                                                    397-8338
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90.9%; Pred. No. 0.029;
tive 0; Mismatches
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       0; Mismatches
                         Score 47; DB 5;
Pred. No. 0.029;
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Matches

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US-08-484-661A-37
                                                                                                                                                                                                     Sequence 37,
                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37,
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                            APPLICANT: Otto, Paul
TITLE OF INVENTION: THERMOPHILIC DNA POLYMERASES FROM
TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 571 amino acid
                                                                                    APPLICANT:
                                                                                                    APPLICANT:
                                                                                                                    APPLICANT:
                                                                                                                                      APPLICANT:
                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                          419 LSVRLGIPVKE 429
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                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                          1 LSVRLGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                     Application US/08656664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 amino acids
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                                                                                  Storts, Douglas R.
                                                                                                  Hartnett, James R. Bolchakova, Elena
                                                                                                                                    Huang, Fen
                                                                                                                                                    Slater, Michael R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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RESULT 9
PCT-US96-09641-37
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               ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diame E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRI
                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THERMOTOGO NEAFOLITANA NUMBER OF INVENTION: THERMOTOGO NEAFOLITANA
NUMBER OF SECUENCES: 57
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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LENGTH: 571 amino acids
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TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         CLASSIFICATION:
                                                                                                        APPLICATION NUMBER: FILING DATE: 31-MAY
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CITY: San Francisco
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                                                                                                                                                                                                                                                          94104
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7: United States Of America
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220 Montgomery Street, Suite 2200
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                                                                                                          31-MAY-1996
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                                                                                                                         PCT/US96/09641
                 PRMG-02185

 Mismatches

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US-08-656-664-11
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                                                                                                                      Matches
                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
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LENGTH: 571 amino acids
TYPE: amino acid
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LENGTH: 578 amino acid
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                              426 LSVRLGIPVKE 436
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Local Similarity 90.98;
nes 10; Conservation
                                                                                                                    hes 10; Conserv
                                                                                         1 LSVRLGXPVKE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: SAN FRANCISCO
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                                                                                                                      Conservative
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                                                                                                                                                                                                          linear
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                                                                                                                                  95.98;
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Pred. No.
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                                                                                                                                  Score 47; DB 3; Pred. No. 0.035;
                                                                                                                      Mismatches
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                                                                                                                    1; Indels
                                                                                                                                               Length 578;
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US-08-656-664-11
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Best Local Similarity
Matches 10; Conserv
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COMPUTER READABLE FORM
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MEDIUM TYPE: Floppy
                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                             TITLE OF INVENTION: THERMOPHILIC DNA POLYM
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                                                                 220 Montgomery Street, Suite 2200
                           United States Of America
                                                                                                                                                        Storts, Douglas R. Otto, Paul
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Hartnett, James R.
                                                                                                                                                                                     Bolchakova, Elena
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                                                                                   Medlen & Carroll
                                                                                                                                           THERMOPHILLC DNA POLYMERASES FROM
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Sequence 11, Application US/08656664 Patent No. 6077664
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                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 40,027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
TITLE OF INVENTION: THERMOTOGA NEAPOLITANA
THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E. REGISTRATION NUMBER: 4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/656,664
FILING DATE: 31-MAY-1996
                                     Application PC/TUS96(9641
                                                                                                                                                                                                                                                                                                                                                               578 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 Montgomery Street, Suite 2200
Slater, Michael R.
                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                              95.98;
90.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elena
                                                                                                                                                                                                                                                                                                                                                                                                       11:
                                                                                                                                                                                                            Score 47; DB 3; Pred. No. 0.035; 0; Mismatches
                                                                                                                                                                                                                                                DB 3; Length 578;
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US-08-484-661A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8,
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Best Local Similarity
                                                                                      TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAME E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
   TYPE: amino acids
TYPE: amino acid
TOPOLOGY: 1;50
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acid
                                                                                                                      REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: PRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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REFERENCE/DOCKET NUMBER: PRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ADDRESSEE: MEDLEN & CARROLL
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TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLATER, MICHAEL R. HARTNETT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
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IBM PC compatible
protein
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Pred. No. 0.035;
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RESULT 15
US-08-484-661A-19
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US-08-484-661A-16
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                                                                                                      Sequence 19, Application US/08484661A Patent No. 6001645
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                                                                                                                                                                                                                                                                                                    Query Match
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GENERAL INFORMATION:
GENERAL INFORMATION:
SLATER, MICHAEL R.
""PURITY JAMES R.
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                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 397-83
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APPLICANT:
APPLICANT: BOLCHÁKOVA, ELENA
TITLE OF INVENTION: MODIFIED THERMOPHILIC DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                         APPLICANT:
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                                      APPLICANT:
                                                                                                                                                                                                       458 LSVRLGIPVKE 468
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                                                                                                                                                                                                                                                                 DB 3; Local Similarity 90.9%; Pred. No. 0.037; es 10; Conservative 0. winners
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                                      HARTNETT, J
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                                                    SLATER, MICHAEL R. HARTNETT, JAMES R.
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                                                                                                                                                                                                                                                                                                                                                                      linear
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90.98;
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Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                    Length 610;
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COUNTRY: UNITED STATES OF AMEXICA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATCHION DATA:
APPLICATION NUMBER: US/08/484,661A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REFERENCE/DOKET NUMBER: PRMG-01175
TELECOMMUNICATION INFORMATION:
TELEPARX: (415) 397-6338
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-661A-19

95.98; SCOTE 47; DB 3; Le
Search completed: January 15, 2003, 12:38:24 Job time: 10.2857 secs
                                                                                                                                                              Query Match 95.9%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FROM THERMOTOGA NEAPOLITANA NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: CALIFORNIA
COUNTRY: CALIFORNIA
                                                                               1 LSVRLGXPVKE 11
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458 LSVRLGIPVKE 468
                                                                                                                                                                Score 47; DB 3; Length 610; Pred. No. 0.037; 0; Mismatches 1; Indels
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Title:

SUMMARIES

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-MODEL-frame+_D2n.model -DEV=xlh
-Q-/cgn2_1/USPTQ_spool/US09823649/runat_14012003_151001_29119/app_query.fasta_1.1393
-DB=\_Geneseq_101002 -OFMT=fastap -SUFF1X=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -SYART=1 -END=-1 -MARRIX=blosum62 -TRANS=bluman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USEE-US09823649 -GCGN_1_1_0_Grunat_14012003_151001_29119 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARR_TIMEOUT=30 -THREADS=1 -XGAPOD=-10 -XGAPDEXT=0.5 -FGAPOD=6 -FGAPEXT=7
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGAPOP=10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                              9: /SIDS2/gcgdata/geneseq/geneseqn embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-cmbl/NA1999.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-cmbl/NA1991.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.BAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/gcnescq/gencseqn-emb1/NA1984.DAT:*
/SIDS2/gcgdata/genessq/geneseqn-emb1/NA1985.DAT:*
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No.
                                                   Key
old_sequence
                                                                                                                                                                                           5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR;
                                                                                                                                              Thermus species sps17.
                                                                                                                                                                                                                                                               Mutant thermostable DNA polymerase pSPSA288.
                                                                                                                                                                                                                                                                                                                            22-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      AAQ24010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ24010 standard; DNA; 1635 BP
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Location/Qualifiers
1..2

SS

ALJGNMENTS

/\*tag=

/note= "nucleotides 4-861 deleted from the native

No.	Score	Match	Length	DB	ID	Description
,	48	96.0	1635	3 :	AAQ24010	Mutant thermostabl
2		6.	68		24	t thermosta
- ω	48	6.	2043		2400	۲.
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y 0	e ate	90.0	1600 009T	, <u>L</u>	AAT76647	
170	лı		1600	, <u>,</u>	AAV65/86	Thermus aquaticus
ر نــ 20 ×	<u>4</u> д	90.0	200	) L	NAV53407	ectide seque
19	45	90.0	1635	<u>.</u> د	AA023998	- 2
20	45		63	ب بن	AAQ24322	Mutant thermostabl
21	45		63	13	AAQ24328	thermostab
22	4.5	90.0	89	21	AAZ29460	Ω.
) L	4 A		89	8 0	AAT47959	Taq polyme
J N A R	A #	90.0	σ	ς α	AAT47961	ant Taq poly
26	45		1686	200	AAX27130	
27	45	90.0	83	20	AAT47960	Mutant Tag nolymer
28	45		89	20	AAX27131	FY3 polymerase cod
2 2	4.0		69	21	AAZ29461	er
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